

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2002, 23:43:29 ; Search time 237.55 Seconds

(without alignments)
8991.124 Million cell updates/sec

Title: US-09-723-676-1

Perfect score: 1244
1 gttgttcacacgtcagtc.....gcattctcctaactctaa 1244

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scoring table: 1736436 seqs, 858457221 residues

Searched: Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
N.Geneseq_032802:*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1244	100.0	1244	22	AAD08531	Human Interleukin-1
2	537.4	43.2	385	22	AAC90487	Human IL-1 eta CDN
3	459	36.9	520	22	AAF83869	Human Interleukin-1
4	324.4	26.1	1190	19	AAV69326	Human IL-1 delta c
5	273	21.9	1304	23	AA594214	DNA encoding novel
6	251.8	20.2	320	19	AAV69327	Human IL-1 delta c
7	134.2	10.8	477	21	AA51247	Human Interleukin-1
8	134.2	10.8	477	21	AA51248	Polymorphic human
9	132	10.6	819	22	AAD06911	Human Interleukin-

10	126.4	10.2	1073	22	AAD12296	Human interleukin-
11	126.4	10.2	1183	19	AAV42659	CDNA encoding inte
12	126.4	10.2	1183	20	AAV90135	Human interleukin-
13	126.4	10.2	1183	22	AA526842	Human CDNA encodin
14	126.4	10.2	1291	20	AA586458	CDNA encoding a hu
15	126.4	10.2	1377	20	AA586459	CDNA encoding a hu
16	119	9.6	673	22	AA526915	Human CDNA encodin
17	119	9.6	673	22	AAD16762	Human novel protei
18	106.8	8.6	811	23	AA594212	DNA encoding novel
19	104.8	8.4	1321	21	AA596351	CDNA encoding a no
20	104.8	8.4	1321	21	AA515950	Human IL-1 recepto
21	100.8	8.1	809	19	AAV1960	Rodent interleukin
22	100.8	8.1	838	20	AA586460	CDNA encoding a mu
23	95.6	7.7	391	22	AAF83870	Human Interleukin-
24	76.2	6.1	654	21	AAD00214	Human zilla4-E200K
25	74.6	6.0	654	21	AAD00213	Human zilla4 degen
26	74.2	6.0	771	23	AA594215	DNA encoding novel
27	73.2	5.9	531	22	AAF85156	Nucleotide sequenc
28	73.2	5.9	603	22	AAF85157	Nucleotide sequenc
29	73.2	5.9	1577	19	AAV21578	Equine interleukin
30	73.2	5.9	1614	22	AAF85155	Nucleotide sequenc
31	72.4	5.8	531	17	AAT13177	Human interleukin-
32	72.4	5.8	557	16	AA089792	IL-1 gene. Homo
33	70.8	5.7	456	14	AA040754	IL-1 inhibitor (IL
34	70.8	5.7	462	18	AA738808	Recombinant human
35	70.8	5.7	462	19	AAV36455	Human Interleukin-
36	70.8	5.7	462	22	AA170513	Human Interleukin-
37	70.8	5.7	514	16	AA083763	Plasmid 15424. Sy
38	70.8	5.7	514	18	AA072210	DNA encoding leade
39	70.8	5.7	514	20	AA582158	Leaderless IL-1 re
40	70.8	5.7	531	17	AAT35255	Human interleukin-
41	70.8	5.7	531	17	AAT30157	Interleukin-1 rece
42	70.8	5.7	531	17	AAT30159	Interleukin-1 rece
43	70.8	5.7	532	12	AA014693	IRAP gene. Homo s
44	70.8	5.7	540	10	AAV2441	Sequence of bps 61
45	70.8	5.7	543	19	AAV22666	CDNA encoding an i

ALIGNMENTS

RESULT 1	
ID	AAD08531 standard; CDNA; 1244 BP.
XX	XX
AC	AAD08531;
XX	XX
DT	04-SEP-2001 (first entry)
XX	XX
DE	Human Interleukin-1 Receptor Antagonist-Like (IL-1ra-L) CDNA.
XX	XX
KW	Human; Interleukin-1 Receptor Antagonist-Like; IL-1ra-L; atherosclerosis;
KW	multiple sclerosis; septic shock; anorexia; psoriasis; osteoporosis;
KW	emphysema; Alzheimer's disease; gene therapy; tranquiliser; vulnerability;
KW	cytostatic; rheumatoid arthritis; autoimmune disease; diabetes; leprosy;
KW	pulmonary tuberculosis; septicemia; cachexia; hypoglycemia; lung injury;
KW	Parkinson's disease; eczema; glomerulonephritis; haemorrhage; ischaemia;
KW	leukaemia; infertility; inflammatory eye disease; acute pancreatitis;
KW	fibromyalgia; ss.
OS	Homo sapiens.
XX	XX
FH	Key
FT	Location/Qualifiers
FT	301...774
FT	/tag= a
FT	/product= "Human IL-1ra-L protein"
PD	WO200142305-A1.
XX	XX
PD	14-JUN-2001.
XX	XX
PF	28-NOV-2000; 2000MO-US32400.
XX	XX

PR	10-DEC-1989;	99US-0170052.
PR	28-NOV-2000;	2000US-0170052.
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Welcher AA, Luethy R, Jing S;	
XX		
DR	WPI; 2001-417857/44.	
DR	P-PSDB; AAE04299.	
XX		
PT	Novel interleukin-1 receptor antagonist-like polypeptide, its fragment,	
PT	variant useful for treating multiple sclerosis, septic shock, anorexia,	
PT	Alzheimer's disease, emphysema, psoriasis, osteoporosis,	
PT	atherosclerosis	
XX		
PS	Claim 1; Fig 1; 133pp; English.	

PD 30-NOV-2000.
 XX 25-MAY-2000; 2000WO-US14435.
 XX 25-MAY-1999; 99US-0135758.
 PR 29-OCT-1999; 99US-0162331.
 XX (IMMV) IMMUNEX CORP.
 XX
 PI Sims JE, Renshaw BR;
 XX
 DR WPI: 2001-032039/04.
 P-PSDB: AAB50444.
 XX
 PT Novel interleukin-1 eta polypeptides useful as therapeutic agents for
 PT treatment of diseases mediated by polypeptide counter-structure
 PT molecules and for identifying inhibitors -
 XX
 PS Claim 1; Page 4; 45pp; English.
 XX
 CC The present sequence encodes an interleukin-1 (IL-1) eta polypeptide.
 CC The IL-1 eta polypeptide is useful as a therapeutic agent for the
 CC treatment of disease mediated by IL-1 eta polypeptide counter-structure
 CC molecules and also for identifying proteins associated with IL-1 eta
 CC ligands, to screen for potential inhibitors of activity associated with
 CC polypeptide counter-structure molecules and in designing inhibitors.
 CC It is used to study cellular processes such as immune regulation, cell
 CC proliferation, cell death, cell migration, cell-to-cell interaction and
 CC inflammatory responses. IL-1 eta promotes inflammatory responses and is
 CC involved in the causation and maintenance of inflammatory and/or
 CC autoimmune diseases such as rheumatoid arthritis, inflammatory bowel
 CC disease, and psoriasis. IL-1 eta polynucleotides can be used to identify
 CC IL-1 eta receptors, to study cell signal transduction and the
 CC immune system and to identify genes associated with human conditions
 CC such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes
 CC mellitus, wrinkly skin syndrome, T-cell leukemia/lymphoma, and tibial
 CC muscular dystrophy.
 CC
 SO Sequence 585 BP; 161 A; 154 C; 110 G; 160 T; 0 other;
 Query Match 43.2%; Score 537.4; DB 22: Length 585;
 Best Local Similarity 98.0%; Pred. No. 8, 6e-153;
 Matches 544; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 220 taacttcgtctgcttagaaccagcctctcaccacatcgtatcctgttctctc 279
 DB 31 tcactctctcctcaacttctcctagcctcctcaccacatcgtatcctgttctctc 90
 QY 280 acaaaagctcgaagacatcatgaaccacaacggaggaagcaaccaccaatcctatgct 339
 DB 91 acaaaagctcgaagacatcatgaaccacaacggaggaagcaaccaccaatcctatgct 150
 QY 340 attcgtgattctcgacagatggtgtgtcctgagtggaatccttataagcagctcct 399
 DB 151 attcgtgattctcgacagatggtgtgtcctgagtggaatccttataagcagctcct 210
 QY 400 cttaaccggaagattaagcctcctccttcttaataagcctgtagaagcagaattc 459
 DB 211 cttaaccggaagattaagcctcctccttcttaataagcctgtagaagcagaattc 270
 QY 460 agtgcagaagaaagggtatatagttacctggtgaatcaagaagaaagtctctgtctc 519
 DB 271 agtgcagaagaaagggtatatagttacctggtgaatcaagaagaaagtctctgtctc 330
 QY 520 ttctgtgcagaatcctcaggaagcactcttgacgtcagcttaagaaataatcatgagac 579
 DB 331 ttctgtgcagaatcctcaggaagcactcttgacgtcagcttaagaaataatcatgagac 390
 QY 580 ctgtatgtgagaagaagacagagcccttctcttccacaataagaagagctcc 639
 DB 391 ctgtatgtgagaagaagacagagcccttctcttccacaataagaagagctcc 450

QY 640 actctgtcttcagtcagtcctcttaccctgctggttcatagaccctccacacatca 699
 DB 451 actctgtcttcagtcagtcctcttaccctgctggttcatagaccctccacacatca 510
 QY 700 ggaacgccatcttcttcacccaagagagagcactaactaactaacttactta 759
 DB 511 ggaacgccatcttcttcacccaagagagagcactaactaactaacttactta 570
 QY 760 gattctgtggaataa 774
 DB 571 gattctgtggaataa 585
 RESULT 3
 AAF83869
 ID AAF83869 standard; cDNA; 520 BP.
 AC AAF83869;
 XX 06-AUG-2001 (first entry)
 DT
 XX
 DE Human interleukin-1 receptor antagonist (NOVINTRA B) encoding cDNA.
 XX
 XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
 KW gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;
 KW cytosolic; neuroprotective; reproductive; antiinflammatory; cancer;
 KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
 KW antisthmatic; antiallergic; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 3..513
 FT /*tag= a
 FT /product= "NOVINTRA B"
 PN WO200140291-A2.
 PD 07-JUN-2001.
 XX
 PF 06-DEC-2000; 2000WO-US33029.
 XX
 PR 06-DEC-1999; 99US-0169056.
 PR 09-DEC-1999; 99US-0169866.
 PR 09-DEC-1999; 99US-0169886.
 PR 10-DEC-1999; 99US-0170252.
 PR 12-JAN-2000; 2000US-0175740.
 PR 05-DEC-2000; 2000US-0170252.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zerhusen BD;
 PI Mezes PS;
 DR WPI: 2001-374790/39.
 P-PSDB: AAB85000.
 XX
 PT Novel isolated human transmembrane, neuromedin peptide
 PT gonadotropin-like protein and interleukin-1 receptor antagonist
 PT proteins, useful for treating cancer, immune response disorder,
 PT metabolic function disorders -
 XX
 PS Claim 8; Fig 12A; 138pp; English.
 XX
 CC The invention provides novel polypeptides (NOVX) selected from human
 CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
 CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
 CC antagonist proteins (NOVINTRA A and B). The invention also provides
 CC methods in which a NOVX polypeptide, polynucleotide and antibody are
 CC used in the detection, prevention and treatment of a broad range of
 CC pathological states. NOVTRAN can be used to treat a cell signaling
 CC disorder such as cancer, immune response disorder, hematopoietic
 CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat

CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
 CC central nervous system, breast, colon, ovary, kidney, prostate and
 CC thyroid. NOVON can be used to treat reproductive development disorder,
 CC metabolic function disorder and melanoma. NOVONTRA A and B can be used
 CC to treat bone metabolism or structure disorder, inflammatory response
 CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
 CC arthritis and cancer. The present sequence represents a cDNA encoding
 CC the NOVONTRA B polypeptide.

XX Sequence 520 BP; 147 A; 127 C; 112 G; 134 T; 0 other;

Query Match 36.9%; Score 459; DB 22; Length 520;
 Best Local Similarity 100.0%; Pred. No. 5.3e-129;

Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 caccacaatcctatgctatgctgattctgacgaatggtgtggtctctgtgtaatt 382
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 62 caccacaatcctatgctatgctgattctgacgaatggtgtggtctctgtgtaatt 121
 QY 383 cttaatagcagctctctcttaagcagacatlaagcctgtcactcttcaatlaagcct 442
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 122 cttaatagcagctctctcttaagcagacatlaagcctgtcactcttcaatlaagcct 181
 QY 443 gtaggacacgaatcattgacgaagaaaggttaattggtttacctgggaatcaagg 502
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 182 gtaggacacgaatcattgacgaagaaaggttaattggtttacctgggaatcaagg 241
 QY 503 gaaagatctcgtctctctctgacgaatcagggcagcactcttgagcttaagg 562
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 242 gaaagatctcgtctctctctgacgaatcagggcagcactcttgagcttaagg 301
 QY 563 aaaaaataatcagctgtatgtgtgagaagaagacagaaagcccttctcttcc 622
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 302 aaaaaataatcagctgtatgtgtgagaagaagacagaaagcccttctcttcc 361
 QY 623 acaataaagaagcctcctctctctgacgaatcagggcagcactcttgagcttaagg 682
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 362 acaataaagaagcctcctcctctctgacgaatcagggcagcactcttgagcttaagg 421
 QY 683 ccaactccacacatcagacagcagccatcttccacaaagagagaggaactaata 742
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 422 ccaactccacacatcagacagcagccatcttccacaaagagagaggaactaata 481
 QY 743 acactaacttacttagattctgtggaataatccagc 781
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 482 acactaacttacttagattctgtggaataatccagc 520

RESULT 4

AAV69326 standard; cDNA; 1190 BP.

AAV69326;

08-FEB-1999 (first entry)

Human IL-1 delta cDNA.

XX Interleukin-1; IL-1 delta; human; diagnosis; immunise; vaccine; stroke;
 XX inoculate; inflammation; arthritis; septicemia; autoimmune disease;
 XX inflammatory bowel disease; psoriasis; transplant rejection; infection;
 XX graft versus host disease; ischemia; acute respiratory disease syndrome;
 XX restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer;
 XX lymphoproliferative disorder; atherosclerosis; Alzheimer's disease;
 XX mapping; linkage; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS

XX 112..606
 XX /*tag= a
 XX /product= "IL-1 delta"

XX EP879889-A2.

XX 25-NOV-1998.

XX 17-FEB-1998; 98EP-0301169.

XX 29-SEP-1997; 97US-0939300.

XX 19-MAY-1997; 97US-0046957.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX Connor JR, James IE, Young PR;

XX WPI: 1998-596881/51.

XX P-PSDB; AAW62542.

XX New IL-1 delta polypeptide and polynucleotide - useful as diagnostic

XX reagents and for diagnosing, prevention or treatment of cancer, AIDS

XX or Alzheimer's disease

XX Claim 2; Page 17; 21pp; English.

This sequence encodes a novel human interleukin-1 polypeptide, IL-1
 delta, (interleukin-1 delta). IL-1 delta polypeptides and
 CC polynucleotides are useful for diagnosing susceptibility to diseases
 CC by detecting mutations in the IL-1 delta gene. IL-1 delta antibodies
 CC are useful for inducing an immune response to immunise and prevent
 CC diseases, and for isolating IL-1 delta clones or purifying the
 CC polypeptides by affinity chromatography. IL-1 delta polypeptides can
 CC be administered directly or as a vaccine to inoculate against disease.
 CC Diseases diagnosed, prevented or treated include: chronic and acute
 CC inflammation, arthritis, septicemia, psoriasis, autoimmune diseases e.g.
 CC inflammatory bowel disease, stroke, ischemia, acute respiratory disease
 CC host disease, infection, stroke, psoriasis, transplant rejection, graft versus
 CC syndrome, restenosis, brain injury, AIDS, bone diseases e.g.
 CC osteoporosis, cancer e.g. lymphoproliferative disorders, atherosclerosis
 CC and Alzheimer's disease. The IL-1 delta polypeptide is also useful for
 CC mapping the gene to a chromosome, allowing gene inheritance to be studied
 CC through linkage analysis.

Sequence 1190 BP; 371 A; 227 C; 251 G; 341 T; 0 other;

Query Match 26.1%; Score 324.4; DB 19; Length 1190;

Best Local Similarity 96.8%; Pred. No. 6.4e-88;

Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctgcttagaacaccagcctctccacacatctgattctatcttctctc 279
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 31 tcacctctccttcaacttctctagcctctccacacacatctgattctatcttctctc 90
 QY 280 acaaaagcctctgaagacatcagaaacacaaagggagagcagacacccaatcctatgct 339
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 91 acaaaagcctctgaagacatcagaaacacaaagggagagcagacacccaatcctatgct 150
 QY 340 attcgtatctctgacagatggtgtggtcctgagtggaattcttaataagcactct 399
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 151 attcgtatctctgacagatggtgtggtcctgagtggaattcttaataagcactct 210
 QY 400 cttagcgcagacatlaagcctgtcaactctcaatttaataagcctgttagagacagaatc 459
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 211 cttagcgcagacatlaagcctgtcaactctcaatttaataagcctgttagagacagaatc 270
 QY 460 agtgacaagaaaggttaattggtttacctggtggaatcaaggaaagatctgtctc 519
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 271 agtgacaagaaaggttaattggtttacctggtggaatcaaggaaagatctgtctc 330
 QY 520 ttctgtgcagaaattcagggcagcactcttgagcttaag 561
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 331 ttctgtgcagaaattcagggcagcactcttgagcttaag 372

CC be administered directly or as a vaccine to inoculate against disease.
 CC Diseases diagnosed, prevented or treated include: chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune diseases e.g.
 CC inflammatory bowel disease, psoriasis, transplant rejection, graft versus
 CC host disease, infection, stroke, ischemia, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases e.g.
 CC osteoporosis, cancer e.g. lymphoproliferative disorders, arteriosclerosis
 CC and Alzheimer's disease. The IL-1 delta polypeptide is also useful for
 CC mapping the gene to a chromosome, allowing gene inheritance to be studied
 CC through linkage analysis.
 XX
 SQ Sequence 320 BP; 80 A; 81 C; 61 G; 91 T; 7 other;

Query Match 20.2%; Score 251.8; DB 19; Length 320;
 Best Local Similarity 93.8%; Pred. No. 3.6e-66;
 Matches 270; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
 QY 220 taactctctgcttgaaccgctcctccacacacatctgcttctctc 279
 Db 23 taacctctcttcaacttctcctcctccacacacatctgcttctctc 82
 QY 280 acaaaagctctgaagacatcatgaaccacaagggagggagcccaatccatgct 339
 Db 83 acaaaagctctgaagacatcatgaaccacaagggagggagcccaatccatgct 142
 QY 340 attctgtt-attctgcagacagatggtgtgtgtcctgtgagtggaattcttaataagcagctcc 398
 Db 143 attctgttattcttgcagacagatggtgtgtgtcctgtgagtggaattcttaataagcagctcc 202
 QY 399 tctttagccgacgataaagcctgtcaactcttcaatttaataagcgttagagacagaatt 458
 Db 203 tctttagccgacgataaagcctgtcaactcttcaatttaataagcgttagagacagaatt 262
 QY 459 cagtgacaagaaagggataatgtgttccctgtgggaatcaaggga 506
 Db 263 cagtgacaagaaagggataatgtgttccctgtgggaatcaaggga 310

RESULT 7
 AAZ51247
 ID AAZ51247 standard; DNA; 477 BP.
 XX
 AC AAZ51247;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Human Interleukin-1 epsilon DNA.
 XX
 KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
 KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
 KW gene mapping; immune system; treatment; inflammatory disease;
 KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
 KW psoriasis; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1.477
 FT CDS /tag= a
 FT /product= "Interleukin-1 epsilon protein"
 XX /note= "Homologous to mouse IL-1 epsilon protein"
 XX
 PN W0200011174-A1.
 XX
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-US18771.
 PF
 XX 21-AUG-1998; 98US-0097413.
 PR 31-AUG-1998; 98US-0098595.
 PR 11-SEP-1998; 98US-0099974.
 XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI SImS JE, Smith DE;
 XX
 DR WPI; 2000-237653/20.
 DR P-PSDB; AAY70217.
 XX
 PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
 PT treat inflammatory and immune system-related diseases such as
 PT rheumatoid arthritis and inflammatory bowel disease -
 XX
 PS Claim 1a; Fig 1; 76bp; English.
 XX

CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA
 CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and
 CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte
 CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
 CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
 CC activity. The DNA sequence can be used in chromosome identification,
 CC gene mapping and study of immune system. IL-1 epsilon can be used in the
 CC treatment of inflammatory or autoimmune diseases such as rheumatoid
 CC arthritis, inflammatory bowel disease and psoriasis.
 XX
 SQ Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 10.8%; Score 134.2; DB 21; Length 477;
 Best Local Similarity 56.8%; Pred. No. 2.4e-30;
 Matches 247; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 340 attctgtattctgcagacagatgtgtgtgtcctgtgagtggaattcttaataagcagctcc 399
 Db 43 attcagatatcatcatcgcgtgtgtgtgttcttcagagacagcgtcatagagcccg 102
 QY 400 cttagccgcagcattaaagcctgtcaactcttcaatttaataagccttagagacagaattc 459
 Db 103 aggaagagccgtatgtctccagctcaacttgccttcaattcattccgacatgtggagacc 162
 QY 460 agtgacaagaaagggataatgtgttccctgtgggaatcaagggaatcaatctctctc 519
 Db 163 cttagaagaaaggaagaaacccatctaccctggcctgaaatgaatcaatctctctc 222
 QY 520 tctgtgcagaaattcgggcaagcctactctgtcagcttaagaaataatcaagcagc 579
 Db 223 atgtgtgctaaagtcgggaccagccacacgcagctgaaagaaagataatagat 282
 QY 580 ctgtatgtggaagaaagcagcagaagcccttctcttccacaataaagaagctcc 639
 Db 283 ttgtacaaccaaccggagcctgtgaaagctcttcttaccacagcagagtggcag 342
 QY 640 acttctgtcttcagtcagctcttaccctgtgctgttcataagcaccctccacacatca 699
 Db 343 aactccaccttgagctgtgtgtcttccctgtgttcattcatgcgtcgcctgaaaga 402
 QY 700 ggaacagccatcttctcaccagaagagagacataactaataacataacttactacta 759
 Db 403 ggcgtctctcatcctcaccacaaagaaactgggaaagcaacactgactgattggtta 462
 QY 760 gatctgtggaata 774
 Db 463 acctatgctgttttaa 477

RESULT 8
 AAZ51248
 ID AAZ51248 standard; DNA; 477 BP.
 XX
 AC AAZ51248;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Polymorphic human Interleukin-1 epsilon DNA.
 XX

(IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or ameliorating IL-1ra-L polypeptide-related disease, condition or disorder which include rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, autoimmune disease, multiple sclerosis, lupus, diabetes, transplant rejection, inflammatory joint disease, graft versus host disease and inflammatory conditions resulting from strain, sprain, cartilage damage, trauma, orthopedic surgery, hepatitis, human immunodeficiency virus (HIV) infection, clostridium-associated diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity, anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory disorders, acute respiratory disease syndrome, cystic fibrosis, asthma, psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis, Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis, lymphomas, lung and breast cancer, leukaemias, infertility, endometriosis, retinal degeneration, retinal neuropathy, acute pancreatitis and Kawasaki's disease.

Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 10.6%; Score 132; DB 22; Length 819;
Best Local Similarity 57.1%; Pred. No. 1.5e-29;
Matches 240; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

```

QY 340 attcgatgattctcgacagatggtgtgtcctgaagtggaattcttaataagcagctcct 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 attcagatattcaatcattcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 cttagccgacagcattagcctgtctcattcattatgacctgttagagacagaattc 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 448 aggaagagccgtatgtctccagcactattgtcattatctcctcagacatgtggagacc 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 aggcagaggaagaaaggaatattgttaccctgggaatcagaagaaagatctctctc 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 508 ctggagagaagacagagggagaccctcactcctggcctggaatcagatcaatccctgtc 567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 tctctgacagaattcaggaggaagcctccttgcagcttaagaaataataatcagagac 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 568 atgtgtcttaagtcgggaccacccacacgcagctgaagaaagataataatgagat 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 580 ctgtatgtggaagaagacagcagcagccttctcttccacataataagaagctcc 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 628 ttctacaaccaacccgagccgtggaagctctctctcaccacagcagagtgagcag 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 actctgtcttctcagctcagctcttaccctgtgtgttcataagccaccacacatca 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 688 aactccacctcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 700 ggcagcagccctcttccaccacagagagagacataactataactacttactta 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 748 ggctgtctctctcattccttaccacagaaactgggaagcacaactactgacttggtta 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 10

AAID12296 standard; DNA; 1073 BP.

AAID12296;

16-OCT-2001 (first entry)

Human Interleukin-1epsilon (IL-1epsilon) protein DNA.

Human; Interleukin-1epsilon; IL-1epsilon; Virusoid; hepatotropic; fever;

immunological disorder; tumour; inflammatory disorder; hypoglycaemia;

autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;

psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Key 67..576

XX CDS /tag- a

FT /product- "Human interleukin-1epsilon (IL-1epsilon)"
FT protein"

XX WO200157219-A2.

XX 09-AUG-2001.

XX 01-FEB-2001; 2001WO-US03285.

XX 02-FEB-2000; 2000US-0179638.

XX (SCHE) SCHERING CORP.

XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;

XX WPI; 2001-488886/53.

XX P-PSDB; AAE06656.

XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon

XX polypeptide useful for treating conditions exhibiting abnormal

XX expression of interleukin such as immunological disorders, tumor and

XX allergy

XX Claim 18; Page 86-87; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like

XX molecules and their corresponding nucleic acid sequences, designated

XX as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).

XX IL-1delta and IL-1epsilon are useful for treating conditions exhibiting

XX abnormal expression of the interleukin such as immunological disorders,

XX tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,

XX allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

XX tuberculosis, leprosy, fulminant hepatitis, and viral infections such as

XX HIV). The invention also relates to methods of using the composition

XX containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic

XX utilities. IL-1delta is used as an immunogen for the production of

XX antisera or antibodies specific, e.g., capable of distinguishing between

XX IL-1 family members and an IL-1delta, for the interleukin or its

XX fragment. The purified interleukin is used as a reagent to detect any

XX antibodies generated in response to the presence of elevated levels of

XX expression, or immunological disorders which lead to antibody production

XX to the endogenous cytokine. The invention also contemplates the use of

XX competitive drug screening assays. The present DNA sequence encodes human

XX interleukin-1epsilon (IL-1epsilon) protein.

XX Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;

Query Match 10.2%; Score 126.4; DB 22; Length 1073;
Best Local Similarity 56.7%; Pred. No. 8.5e-28;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

```

QY 338 ctatcgtgattctcgacagatggtgtgtcctgaagtggaattcttaataagcagctc 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 ctatgaatgattgaatcagcagatgtgagcccttcaaggtcagacactgtgagctc 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 ctcttagccgacagcattgaagccttcaactcattatgaagccttgaagacacaaat 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 caggaagtgacagctgtgacccagcagctcgtgtgttatcacaatgacagacag 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 tcagtgacaaggaaggaataatgatttaccctgggaatcagaaggaagacatctgtc 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 ctcttgagcagaagcagagggatcccatatttgggaatccagaatccagaatgtgtc 322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 tctctgacagaattcagggcagccttctgaagcttgaagccttgaagccttgaagcctt 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 tgtatgtgagaaggttggagacagccacattgacgtataaagagcagaatcagtg 382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 578 accgtatgtgagaaggaagacagagcagccttcttcttccacataaagaagagct 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 atcgtatgacccaacccgagccgtgaaaccccttcttctcagtgccaagactgta 442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 ccaactgtcttctcagtcagctcttaccctgtgtgtgtcatagcacctcacaacat 697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Dd 443 ggacctccaccccttgagtctgtgcttcccgactgcttcatctgctctccaaga--- 499
Qy 698 caggacagcccatcttctcaccagaagagagacataactaactaacttctact 757
Dd 500 gagaccagcccatcttctcacttcagacttggagatcatacaacactgcttgaat 559
Qy 758 tagattctgtggaataaataacccagcttag 785
Dd 560 taatatataaagtacactgactcagccctag 587

RESULT 11
AAV42659
ID AAV42659 standard; cDNA; 1183 BP.
XX AAV42659;
XX 14-OCT-1998 (first entry)
XX cDNA encoding Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
XX Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
XX IL-1 beta; inflammatory response; treatment; inflammation; septicemia;
XX cancer; anaemia; arthritis; inflammatory bowel disease;
XX graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
XX acute respiratory disease syndrome; psoriasis; restenosis;
XX traumatic brain injury; acquired immune deficiency syndrome;
XX cachexia; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 75..584
XX FT /tag= a
XX FT /product= IL-1ra-beta
XX
XX EP855404-A1.
XX
XX 29-JUL-1998.
XX
XX 27-JAN-1998; 98EP-0300572.
XX
XX 28-JAN-1997; 97US-0790032.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Young PR;
XX
XX MPI: 1998-389778/34.
XX P-PSDB; AAW63136.
XX
XX New nucleic acid encoding human interleukin-1 receptor antagonist
XX beta polypeptides - and related expression systems, transformed
XX cells, proteins, antibodies, agonists and antagonists, useful for
XX treatment, prevention and diagnosis of inflammation, septicemia,
XX cancer etc
XX
XX Claim 3; Fig 1; 20pp; English.
XX
XX The present sequence encodes human Interleukin-1 receptor antagonist
XX beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in
XX inflammatory responses, and are produced as zymogens which are cleaved
XX upon secretion to yield mature carboxyl terminal 17 kD fragments.
XX IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
XX chronic and acute inflammation, septicemia, cancer, anaemia, arthritis,
XX stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
XX psoriasis, restenosis, traumatic brain injury, acquired immune
XX deficiency syndrome (AIDS) and cachexia. These conditions (or
XX susceptibility to them) may be diagnosed by detecting mutations in the
XX IL-1ra-beta coding sequence analysing a sample for presence or amount
XX of IL-1ra-beta.

```

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XX
SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;
Query Match 10.2%; Score 126.4; DB 19; Length 1183;
Best Local Similarity 56.7%; Pred. No. 8,9e-28;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;
Qy 338 ctattcgtgattctcgcagatgctgtgtgcttgcagcttaagaaatcttaatacagctc 397
Dd 151 ctatcaatgatttgatcaatcagcaagctgtgacccttcagtggtcagaacctgtgtgcagctc 210
Qy 398 ctctagccgcagcatlaagcctgtcactcttcatttaataagctgtagagacagaaat 457
Dd 211 caaggaagtgcacagtgtgaccaccagctcgtgtgttatacatcgaatccagaaatgtgag 270
Qy 458 tcaatgacaggaagaaaggtaataatgtttactctgggaatcaaggaaatagactctgtc 517
Dd 271 ctcttgagcaagcgacagagggatcccatattatttgggaatccagaatccagaaatgtgt 330
Qy 518 tctctgtacagaatctcaggaagcagcactcttgcagcttaagaaataatcatatg 577
Dd 331 tgtattgtgagagaagtttgagagacagccacatgtcagctaaagcgacagatcatg 390
Qy 578 accgtatgtgagagaagaaagacacagagcccttctcttccacaataaagaagct 637
Dd 391 atctgtatgccaacccgcgcgttgaaaccttctcttctacgctgccaagactgtga 450
Qy 638 caactctgtcttctcagtagctcttaccctgtcgtgttcataagcaccctcaccat 697
Dd 451 ggacctccaccccttgagctgtgtgacctcccgagctgtgtcattgctccccaaga--- 507
Qy 698 caggacagcccatcttctcaccagaagagagacataactaactaacttctact 757
Dd 508 gagaccagcccatcttctcacttcagacttggagagatcatacaacactgcttgaat 567
Qy 758 tagattctgtggaataaataacccagcttag 785
Dd 568 taatatataatgactgaactcagccctag 595

RESULT 12
AAV90135
ID AAV90135 standard; cDNA; 1183 BP.
XX
XX AAV90135;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human Interleukin-1 receptor antagonist beta encoding cDNA.
XX
XX Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
XX chronic inflammation; acute inflammation; arthritis; autoimmunity;
XX inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
XX cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
XX traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
XX allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
XX allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO9936541-A1.
XX
XX 22-JUL-1999.
XX
XX 14-JAN-1999; 99WO-US00847.
XX
XX 29-APR-1998; 98US-0069619.
XX 14-JAN-1998; 98US-0007464.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Marshall L, Young PR;
XX

```


clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://baccpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-72533; the clone sequenced to the right is RP11-97914. Actual start of this clone is at base position 1 of RP11-339F22; actual end is at base position 197308 of RP11-339F22.

Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and AC016724.

FEATURES
Source Sequence derived from PCR from base position 148683 to 149264.

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1. 197308
   location/Qualifiers
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /chromosome="2"
   /map="2"
   /clone="RP11-339F22"
   /clone.lib="RPCI-11"
   6. 275
   /rpt_family="L1"
   repeat_region
   /rpt_family="L1"
   274. 740
   /rpt_family="L1"
   repeat_region
   /rpt_family="ERV1"
   744. 907
   /rpt_family="ERV1"
   repeat_region
   917. 1361
   /rpt_family="L1"
   repeat_region
   /rpt_family="L1"
   1362. 1814
   /rpt_family="L1"
   repeat_region
   1838. 1952
   /rpt_family="ERV1"
   repeat_region
   2105. 2161
   /rpt_family="ERV1"
   repeat_region
   2245. 2587
   /rpt_family="L1"
   repeat_region
   2588. 2877
   /rpt_family="Alu"
   repeat_region
   2878. 3244
   /rpt_family="L1"
   repeat_region
   3235. 4195
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   3460. 3481
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   repeat_region
   4311. 4450
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repeat_region 4822. 4957
/rpt_family="MER1_type"
repeat_region 5152. 5337
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repeat_region 6118. 7901
/rpt_family="L2"
repeat_region 8008. 8145
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repeat_region 8146. 8343
/rpt_family="MER1_type"
repeat_region 8344. 8429
/rpt_family="L2"
repeat_region 8661. 8827
/rpt_family="ERV1"
repeat_region 8999. 9029
/rpt_family="Tn"
9003. 9030
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9011. 9031
/note="similar to Homo sapiens EST AA587127 (NID:g23397941) n70c01.s1"
9013. 9031
/note="similar to Homo sapiens EST A1034379 (NID:g23255332) ox20911.x1"
9167. 9564
/rpt_family="L2"
repeat_region 10187. 10267
/rpt_family="MIR"
11074. 11122
/rpt_family="(CTG)n"
11587. 11611
/rpt_family="(TG)n"
11651. 11884
/rpt_family="MALR"
12198. 12353
/rpt_family="MIR"
12578. 12714
/rpt_family="MER1_type"
13540. 13855
/rpt_family="Alu"
13985. 14843
/rpt_family="L1"
14923. 15243
/rpt_family="MER2_type"
15980. 16836
/rpt_family="L1"
17526. 17822
/rpt_family="Alu"
18067. 18089
/rpt_family="AT-rich"
19365. 19493
/rpt_family="MER1_type"
19604. 20083
/rpt_family="ERV1"
20084. 20447
/rpt_family="MALR"
20448. 21020
/rpt_family="ERV1"
21033. 21306
/rpt_family="L1"
21315. 21656
/rpt_family="ERV1"
21906. 22079
/rpt_family="ERV1"
22533. 22637
/rpt_family="MER2_type"
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23345. 23852
/rpt_family="L1"
25801. 25931
/rpt_family="ERV1"
repeat_region
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kubin,M., Garika,K.E. and Sims,J.E.
TITLE Four new members expand the interleukin-1 superfamily
JOURNAL J Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
REFERENCE 2 (bases 1 to 585)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES
SOURCE
1..585
/organism="Homo sapiens"
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/chromosome="2"
/map="2q: between D2S121 and D2S110"
112..585
/note="similar to IL-1"
/codon_start=1
/product="FIL1 eta"
/protein_id="AAF25213.1"
/db_xref="GI:6694394"
/translation="MNPOREAPKSYAIRDSRQWVVLGNSLIAPLSRSIKPYTLH LIAKRDIFSDKREKNMYLIGIKKDLDFCEIOGKPTQIKENIMLYEKKOK PFLFHNEGSTVSFQSVSPQWFIATISGQPLFLTKERGITNNINFLDSVE"
BASE COUNT 161 a 154 c 110 g 160 t
ORIGIN

Query Match 43.2%; Score 537.4; DB 9; Length 585;
Best Local Similarity 98.0%; Pred. No. 7,5e-141;
Matches 544; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctcttagaaccaccctctctcaccacatctgatacttctctctc 279
DB 31 TCACCTCTCCTTCTACTTTCTTCTAGCTCTCTCACCACATGTGATCTTGTCTCTTC 90
QY 280 acaaaagctctgaagacatcatgaaccacaacggaagcagcaaccacaactctatgct 339
DB 91 ACAAAGGCTTGAAGACATCATGACCAACGAGGAGGACACCAATCCTATGCT 150
QY 340 atctgtatcttcgaaagtgtgtgtgtctctgagtgagaaatctttaaagagccct 399
DB 151 ATTCTGATTCGACAGATGCTGTGGTCTGATGGAATTCCTTAATGACAGCTCT 210
QY 400 cttagccgacgaactaagcctgtcactcttcatltaataagcctgtagagacagaattc 459
DB 211 CTTAGCCGACGATTAAGCTGTGACTCTTCACTTAATACCTGTATAGACACGAATTC 270
QY 460 agtgaagaagaagaaggtaatatgttacctgaggaaatcaagggaaaagatctctctc 519
DB 271 AGTAGCAAGAAAGAGTATATGTTACCTGGAAATCAAGGGAAAGATCTCTGCTC 330
QY 520 tctctgtcgaagaattcaaggcaagcctactcttgacgttaagaaaaaataatcatgagc 579
DB 331 TTCTGTGAGAAATTCAGGGCAAGCTTCTTCACTTAAGGAAAAAATATCATGGAC 390
QY 580 ctgtaagtgaagaagaagacagaagccttctctcttctccacaataaagaagctcc 639
DB 391 CTGTATGTGAGAAAGAGACAGAACCCCTTCTCTTTTCCACATTAAGAAGGCTCC 450
QY 640 acttctgctcttcaagtcctcttacctgctgtgttcatagccactccacacatca 699
DB 451 ACTTCTGTCTTCACTGACGCTCTTACCTGGCTGTTCATAGCCACCTCCACACATCA 510
QY 700 gggacacccactcttctcacaagggagagagcaataactaataacactaacttacta 759
DB 511 GGACAGCCCATTTTCTCACCAAGAGAGAGGCTAATACTAATACTTACTTACTTA 570

QY 760 gatctctggaataa 774
DB 571 GATTCTGTGAATTA 585

RESULT 5
LOCUS AX193587 520 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 9 from Patent WO0140291.
ACCESSION AX193587
VERSION AX193587.1 GI:15211517
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L., Zerhusen,B.D. and Mezes,P.S.
TITLE Proteins and nucleic acids encoding the same
JOURNAL Patent: WO 0140291-A 9 07-JUN-2001; Curagen Corporation (US)
FEATURES
SOURCE
1..520
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 147 a 127 c 112 g 134 t
ORIGIN

Query Match 36.9%; Score 459; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 caccacaatctatgctcttctgctgcttcgcacagatggtggtggtccgagtgaaatt 382
DB 62 CACCAAAATCCTATCTATCTGCTGATTTCTCGACAGATGCTGTGGTCTCGAGCGAAAT 121
QY 383 cttaatagcagctctctcttagccgacgataagcctgtcacctcttcaatagcct 442
DB 122 CTTTATATGACAGCTCTCTTACCCGACGATTAAAGCTGTCACTTCAATTAATGACCT 181
QY 443 gttagagacagaattcagtgacaaggaaggtatatagttttaccctggagaaataag 502
DB 182 GTAGAGACACAAATTCAGTGAAGGAAAGGTATATGTTTACCTGGGAATCAAG 241
QY 503 gaaagatctctgtctctctctgtgcagaatcaaggaagcctactcttgcaactaaag 562
DB 242 GAAAAGATCTCTGTCTCTCTGTGCAAGAAATTCAGGGCAAGCTTACTTTCACCTTAAG 301
QY 563 aaaaaatacatgagacctgtaagtgtgagaagaagacagaagcccttctcttctcc 622
DB 302 AAAAAATATCATGAGACCGTGTATGTGAGAGAAGAAACACAGAACCCCTTCTCTTTTCC 361
QY 623 acaataaagaagctccactctgtctcttcaagtcagtccttcttaccctgctggttcaag 682
DB 362 ACAATTAAGAAAGGCTCCACTTCTGTCTTTCAGTCACTCTCTTACCCCTGGCTGTTATAG 421
QY 683 ccactctcacacatcagacagcagccacttcttccacaaggaagagacataactaata 742
DB 422 CCACCTCCACCAATCAGACAGCCCATCTTTTCTCCACAAAGAGAGACATTAATAATA 481
QY 743 acaataacttacttagattctgtggaataaattccagc 781
DB 482 ACAGTAACCTTACTTAGATTCGTGGAATTAATTCAGC 520

RESULT 6
LOCUS AX193643 329 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 65 from Patent WO0140291.
ACCESSION AX193643

VERSION AX193643.1 GI:15211536
KEYWORDS
SOURCE
ORGANISM Sus scrofa
REFERENCE Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
AUTHORS 1 (bases 1 to 329)
TITLE Burgess, C.E., Prayaga, S.K., Shinkets, R.A., Rastelli, L.,
Zeihusen, B.D., and Mezes, P.S.
JOURNAL Proteins and nucleic acids encoding the same
Patent: WO 0140291-A 65 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..329
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 103 a 77 c 64 g 85 t
ORIGIN

Query Match 26.4%; Score 329; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.1e-82;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 catttaataagcctgttagagacacagaattcagtgacaaaggaaggtaatatgtttac 489
-DB 1 CATTAATAAGCCTGTAGAGACACAGATTCTAGTACAAAGGAAGGTAATATGTTTAC 60
QY 490 ctgggaataaggaagaagatctctctctctctgtgcagaataatcagggaagcctact 549
DB 61 CTGGGAATCAAGGAAAGATCTCTCTCTCTCTGTGCAGAAATTCAGGGCAACCTACT 120
QY 550 ttgcagcttaaggaagaagaatatacatgacactgtatgtgagaagaagaacagagcc 609
DB 121 TTGCAGCTTAAGGAAAAAATATCATGACCTGTATGTGAGAAAGACACAGAGCC 180
QY 610 ttctctcttcccaataaagaagctcactctgtctcttcaagtcagtccttaccct 669
DB 181 TTCTCTTTTCCCAATAAAGAGGCTCCTCTCTCTTTCAGTCACTCTTACTTACT 240
QY 670 gctctgttcataagcactccacacatcagaagagccactcttctcacaagaagagaga 729
DB 241 GGCTGTTCATAGCCACCTCCACCATCAGGACAGCCCATCTTTCTCACCAGAGAGAGA 300
QY 730 ggcaataactaataactaacttactt 758
DB 301 GGCAATACTAATAACACTACTTACTT 329

RESULT 7
LOCUS E28610 1190 bp DNA linear PAT 07-FEB-2001
DEFINITION Novel member of IL-1 family, IL-1-delta.
ACCESSION E28610
VERSION E28610.1 GI:13025428
KEYWORDS JP 1999000177-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1190)
AUTHORS Peter, R.Y.I.I. and James, J.R.C.C.
TITLE Novel member of IL-1 family, IL-1-delta
JOURNAL Patent: JP 1999000177-A 1 06-JAN-1999;
SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 1999000177-A/1
PD 06-JAN-1999
PE 16-JAN-1998 JP 1998007091
PR 19-MAY-1997 US 60/046957, 29-SEP-1997 US 08/939300 PI
PETER R YOUNG, IAN E JAMES, JANICE R CONNER
PC C12N15/09, A61K38/00, A61K38/00, A61K38/00, A61K38/00,
A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K39/395, A61K39/395,

PC A61K48/00,
PC C07K14/545, C07K16/24, C12P21/02, C12Q1/68, C12N15/09, C12R1/91,
PC C12N15/00,
PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02,
PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02,
PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02,
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..1190
/organism="Unidentified".
FEATURES
source Location/Qualifiers
1..1190
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 371 a 227 c 251 g 341 t
ORIGIN

Query Match 26.1%; Score 324.4; DB 6; Length 1190;
Best Local Similarity 96.8%; Pred. No. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctcttagaaccagccctccacacacatcatatcttctcttc 279
DB 31 TCACTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 90
QY 280 acaaaagctctgaagacatcgaaccacaacagagagagacacccaactatgct 339
DB 91 ACAAAAGGCTCTGAMGACATCATGACCACACAGGAGGAGCAGCACCAATCTATGCT 150
QY 340 atcgtgatctctgacagatggttggtgctggtgagaaattcttataagactct 399
DB 151 ATTCTGATTTCTGACAGATGCTGTGGTCTGAGTGAATCTTTATATGACACTCT 210
QY 400 cttagccgcagcatlaagcctgtcactcttcaatlaagcctgtagagacagaaatc 459
DB 211 CTTAGCCGCGAGCATTTAGCCTGTGCTCTTCACTTTAATAGCTGTAGAGACAGAAATTC 270
QY 460 agtgacagaagaaggtaatatgtttactctggaatcaagaagaatctctctc 519
DB 271 AGTGACAGAGAAAGGTAATATGTTTACTCTGGAAACAAGGAAAGATCTGTCTC 330
QY 520 ttctgtcagaatcagagcagcctactcttgagcttaag 561
DB 331 TTCTGTGCAGAATTCAGGCAAGCTTACTTTGCACTTAAG 372

RESULT 8
LOCUS E41358 1190 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel member of IL-1 family, IL-1delta.
ACCESSION E41358
VERSION E41358.1 GI:18625169
KEYWORDS JP 2000083688-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1190)
AUTHORS Young, P.R., James, I.E. and Conner, J.R.
TITLE Novel member of IL-1 family, IL-1delta
JOURNAL Patent: JP 2000083688-A 1 28-MAR-2000;
SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 2000083688-A/1
PD 28-MAR-2000
PE 01-SEP-1999 JP 1999247635
PR 19-MAY-1997 US 60/046957, 29-SEP-1997 US 08/939300 PI
PETER R YOUNG, IAN E JAMES, JANICE R CONNER
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P29/00,
A61P35/00,
PC A61P37/02, C07K14/545, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,

PC C12P21/02,C12Q1/02,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;

Location/Qualifiers
FH Key 1..1190
FT source
/organism='Unidentified'.

FEATURES
source 1..1190
/organism='unidentified'
/db_xref='taxon:32644'

BASE COUNT 371 a 227 c 251 g 341 t
ORIGIN

Query Match 26.1%; Score 324.4; DB 6; Length 1190;
Best Local Similarity 96.8%; Pred. No. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctgcttagaaccagcctcctcaaccatctgatactctgtctctc 279
DB 31 TCACCTCTCCTTCACTTTCTTACGCTCCTCACCACCATCTGATCTTCTCTTC 90
QY 280 acaaaaggctctgaagacatcatgaaccacaacgggagcgagcaccacaatctatgct 339
DB 91 ACAAAGGCTCTGAAGACATCATGAACCCACAACGGGAGGAGCACCACCAATCTATGCT 150
QY 340 attcgtatctcgcagacatggtgtgtgtcctgaagtgaatctttaaagacagctcct 399
DB 151 ATTCTGATTTCTGACAGATGAGTGTGTGCTCTGATGGAATCTTTAATAGCAGCTCCT 210
QY 400 cttaagcgcagacatlaagcctctcctctcaatcttaataagcctgtagagacagaattc 459
DB 211 CTTAGCCGAGCATTAAGCTGTCACTCTTCAATTAACCTGTAGAGACAGCAATTC 270
QY 460 agtgacaaggaaggggtatataatgattaccctgggaatcaagggaaaagatctctgtc 519
DB 271 AGTGACAAAGGAAGGGATATATGTTTACCTGGGATCAAGGGAAAAGATCTCTGTCTC 330
QY 520 ttctgtgcagaattcaaggcaagcctactcttgacgcttaag 561
DB 331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTCAGCTTAAG 372

RESULT 9
AF200494 1190 bp mRNA linear PRI 11-MAY-2000
LOCUS AF200494 Homo sapiens interleukin-1 homolog 2 mRNA, complete cds.
DEFINITION AF200494
ACCESSION AF200494.1 GI:7769115
VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1190)
AUTHORS Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
and Young,P.R.
Identification and initial characterization of four novel members
of the interleukin-1 family
J. Biol. Chem. 275 (14), 10308-10314 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

2 (bases 1 to 1190)
Kumar,S., McDonnell,P.C. and Young,P.R.
Direct Submission
Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA
Location/Qualifiers
1..1190
/organism='Homo sapiens'
/db_xref='taxon:9606'

CDS
/tissue_type='osteoclastoma'
112..606
/note='cytokine; hIL-1h2'
/codon_start=1
/product='interleukin-1 homolog 2'
/protein_id='AA69250.1'
/db_xref='GI:7769116'
/translation='MNPQREAPKSYAIRDSRWVWVLSGNSLIAPLSRSIKPYTLH
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LVGIHTFCINLDVRESCEFGITDQWIGVGRKKMKSSFFQHHLRKDKDFSSMTNIGM
PGRW'

BASE COUNT 371 a 227 c 251 g 341 t
ORIGIN

Query Match 26.1%; Score 324.4; DB 9; Length 1190;
Best Local Similarity 96.8%; Pred. No. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctgcttagaaccagcctcctcaaccatctgatactctgtctctc 279
DB 31 TCACCTCTCCTTCACTTTCTTACGCTCCTCACCACCATCTGATCTTCTCTTC 90
QY 280 acaaaaggctctgaagacatcatgaaccacaacgggagcgagcaccacaatctatgct 339
DB 91 ACAAAGGCTCTGAAGACATCATGAACCCACAACGGGAGGAGCACCACCAATCTATGCT 150
QY 340 attcgtatctcgcagacatggtgtgtgtcctgaagtgaatctttaaagacagctcct 399
DB 151 ATTCTGATTTCTGACAGATGAGTGTGTGCTCTGATGGAATCTTTAATAGCAGCTCCT 210
QY 400 cttaagcgcagacatlaagcctctcctctcaatcttaataagcctgtagagacagaattc 459
DB 211 CTTAGCCGAGCATTAAGCTGTCACTCTTCAATTAACCTGTAGAGACAGCAATTC 270
QY 460 agtgacaaggaaggggtatataatgattaccctgggaatcaagggaaaagatctctgtc 519
DB 271 AGTGACAAAGGAAGGGATATATGTTTACCTGGGATCAAGGGAAAAGATCTCTGTCTC 330
QY 520 ttctgtgcagaattcaaggcaagcctactcttgacgcttaag 561
DB 331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTCAGCTTAAG 372

RESULT 10
E28611 320 bp DNA linear PAT 07-FEB-2001
LOCUS E28611 Novel member of IL-1 family, IL-1-delta.
DEFINITION E28611
ACCESSION E28611.1 GI:13025429
VERSION JP 1999000177-A/2.
KEYWORDS
SOURCE
ORGANISM

unclassified.
REFERENCE 1 (bases 1 to 320)
AUTHORS Peter,R.Y.,I.T. and James,J.R.C.C.
TITLE Novel member of IL-1 family, IL-1-delta
JOURNAL Patent: JP 1999000177-A 2 06-JAN-1999;
SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 1999000177-A/2
PD 06-JAN-1999
PE 16-JAN-1998 JP 1998007091
PR 19-MAY-1997 US 60/046957,29-SEP-1997 US 08/939300 PI
PETER R YOUNG, IAN E JAMES, JANICE R CONNER
PC C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
PC A61K38/00
PC A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/395,A61K39/395,
PC A61K48/00
PC C07K14/545,C07K16/24,C12P21/02,C12Q1/68/(C12N15/09,C12R1:91),
PC C12N15/00,
PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,
PC A61K37/02.

COMMENT
PN JP 1999000177-A/2
PD 06-JAN-1999
PE 16-JAN-1998 JP 1998007091
PR 19-MAY-1997 US 60/046957,29-SEP-1997 US 08/939300 PI
PETER R YOUNG, IAN E JAMES, JANICE R CONNER
PC C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
PC A61K38/00
PC A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/395,A61K39/395,
PC A61K48/00
PC C07K14/545,C07K16/24,C12P21/02,C12Q1/68/(C12N15/09,C12R1:91),
PC C12N15/00,
PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,
PC A61K37/02.

PC A61K37/02,A61K37/02,A61K37/02,(C12N15/00,C12R1:91) CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT source
 Location/Qualifiers
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 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 80 a 81 c 61 g 91 t 7 others

ORIGIN

Query Match 20.2%; Score 251.8; DB 6; Length 320;
 Best Local Similarity 93.8%; Pred. No. 4.1e-60;
 Matches 270; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 220 taactctgctgcttagaaccagcctcctcaccacatctgatactctgtctctc 279
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 Db 23 TCACCTNCTTCACCTTTCCTAGCCCTCCTACCATCTGATCTATCTGTCTTC 82

QY 280 acaaaagctcgaagacatcatgaaccacaagaggaagagagacacccaatctatgct 339
 |||||
 Db 83 ACAAAAGCTCTGAGACATCATGACCCACACGAGGAGGACGACCAANTCTATGCT 142

QY 340 attcgtg-attctcgacagatggtggtgctcctgagtggaattcttaataagacgtcc 398
 |||||
 Db 143 ATTGCTGATTTCTNGACAGATGCTGTGGTCTGAGTGAATTTTAAATAGCAGCTTC 202

QY 399 tcttagccgcaacatataagcctgctcctctcatttaataagcctgtagaagacagaatt 458
 |||||
 Db 203 TCTTAGCCGACCATTAACCTGTCTCCTTCACTTAAATAGCCCTGAGACACAGAAAT 262

QY 459 cagtgacaagaaaaggtataatggtttacccggaatacaagagaaa 506
 |||||
 Db 263 CAGTGACAGAGAAAAGGTATATGTTTACCTGGGATCAAGGGAAA 310

RESULT 11
 E41359 320 bp DNA linear PAT 31-JAN-2002
 LOCUS Novel member of IL-1 family, IL-1delta.
 DEFINITION E41359
 ACCESSION E41359.1 GI:18625170
 VERSION JP 2000083688-A/2.
 KEYWORDS unidentified.
 SOURCE unidentified.
 ORGANISM unclassified.
 unclassified.
 1 (bases 1 to 320)
 REFERENCE Young,P.R., James,I.E. and Conner,J.R.
 AUTHORS Novel member of IL-1 family, IL-1delta
 TITLE Patent: JP 2000083688-A 2 28-MAR-2000;
 JOURNAL SMITHKLINE BEECHAM CORP
 COMMENT OS Unidentified
 PN JP 2000083688-A/2
 PD 28-MAR-2000
 PF 01-SEP-1999 JP 1999247635
 PR 19-MAY-1997 US 60/046957,29-SEP-1997 US 08/939300 PI
 PETER R YOUNG,IAN E JAMES,JANICE R CONNER
 PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P29/00,
 PC A61P35/00,
 PC A61P37/02,C07K14/545,C07K16/24,C12N1/15,C12N1/19,C12N1/21, PC
 C12N5/10,
 PC C12P1/02,C12Q1/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/00 CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT source
 Location/Qualifiers
 1..320
 /organism="unidentified".
 Location/Qualifiers
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 /organism="unidentified"

BASE COUNT 80 a 81 c 61 g 91 t 7 others

ORIGIN

Query Match 20.2%; Score 251.8; DB 6; Length 320;
 Best Local Similarity 93.8%; Pred. No. 4.1e-60;
 Matches 270; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 220 taactctgctgcttagaaccagcctcctcaccacatctgatactctgtctctc 279
 |||||
 Db 23 TCACCTNCTTCACCTTTCCTAGCCCTCCTACCATCTGATCTATCTGTCTTC 82

QY 280 acaaaagctcgaagacatcatgaaccacaagaggaagagagacacccaatctatgct 339
 |||||
 Db 83 ACAAAAGCTCTGAGACATCATGACCCACACGAGGAGGACGACCAANTCTATGCT 142

QY 340 attcgtg-attctcgacagatggtggtgctcctgagtggaattcttaataagacgtcc 398
 |||||
 Db 143 ATTGCTGATTTCTNGACAGATGCTGTGGTCTGAGTGAATTTTAAATAGCAGCTTC 202

QY 399 tcttagccgcaacatataagcctgctcctcatttaataagcctgtagaagacagaatt 458
 |||||
 Db 203 TCTTAGCCGACCATTAACCTGTCTCCTTCACTTAAATAGCCCTGAGACACAGAAAT 262

QY 459 cagtgacaagaaaaggtataatggtttacccggaatacaagagaaa 506
 |||||
 Db 263 CAGTGACAGAGAAAAGGTATATGTTTACCTGGGATCAAGGGAAA 310

RESULT 12
 AF201831 477 bp mRNA linear PRI 16-JAN-2000
 LOCUS Homo sapiens F111 epsilon mRNA, complete cds.
 DEFINITION AF201831
 ACCESSION AF201831
 VERSION AF201831.1 GI:6694389
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 477)
 REFERENCE Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kublin,M., Garika,R.E. and
 AUTHORS Sims,J.E.
 TITLE Four new members expand the interleukin-1 superfamily
 JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
 MEDLINE 20092888
 REFERENCE 2 (bases 1 to 477)
 AUTHORS Sims,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
 University Street, Seattle, WA 98101, USA
 COMMENT location/Qualifiers
 1..477
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2q: between D2S121 and D2S110"
 1..477
 /note="similar to IL-1"
 /product="F111 epsilon"
 /codon_start=1
 /product="F111 epsilon"
 /protein_id="AA25211.1"
 /db_xref="GI:6694389"
 /translation="MEKALKIDTPQGSIDINHRVWLDQDTLIAVPRKDMSPVTI
 ALISCHVELENDKGNPIYLINGNLCLMCAKVGDPYQLLEKEDIMDYINPEPV
 KSLFLYHSQSGRSTFESVAFPMWFLIVSSEGGCLPILITQELGRANTDFGLTMLF"

BASE COUNT 124 a 123 c 117 g 113 t

ORIGIN

Query Match 10.8%; Score 134.2; DB 9; Length 477;
 Best Local Similarity 56.8%; Pred. No. 7.2e-27;

Matches 247; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY	340	attctgcatctctgcacagatggtgtgggtcctgaatgtgaaattcttctaatagcagctcct	399
Db	43	ATTGAGATATCAATCAATCGGGTGTGGGTTCTTCAGACCGAGCGTCAATCGAGTCCG	102
QY	400	cttagcgagcaattaaagccctgtcacctcttcatttaatagtcgttagaacagaattc	459
Db	103	AGGAAGAGCCGTATGTCTCCAGTCACTATTGCCATTATTCATGCCAGCATGTGGAGACC	162
QY	460	agtgacaagaaaaggtaabatggtttacctgttggaatcaaaggaagaaatctctgtc	519
Db	163	CTTGAGAAAGACAAGGGAACCCCATCTACTCTGGGCGCTGAATGAGACTCAATCTCGCTG	222
QY	520	ttctgttcagaattcaagggcaagccacttttgagcttaagcttaagaaaaataatcagac	579
Db	223	ATGTGTCTTAATGTGGGGACCCAGCCACACTGCAGCTGAAGGAAAAGATATATGAT	282
QY	580	ctgtatgttggaagaaagacacagaagcccttctctttccacaataaagaagctcc	639
Db	283	TTGTACAACCAACCCGAGCCTGTGAAGCTTTTCTCTCAACAGCCAGAGTGGAGG	342
QY	640	aactctgtcttcaagtcagtcctcttaacctgtgctggttcatagccaactccaacacatca	699
Db	343	AACTCACACTTCGATGCTGNGGCTTTCCCTGGCTGTATCGCTGTAGCTCTGAAGA	402
QY	700	ggaacagccatcttctcacaagaagaaaggaactaaataaacaactaacttactacta	759
Db	403	GGCGTCTCTCACTACCTTACCCAGAAGAACTGGGGAAGCAACACTACAGACTTGGGTTA	462
QY	760	gattctgttgaataa 774	
Db	463	ACTATGCTGTTTAA 477	

RESULT 13
AX207820

LOCUS	1073 bp	DNA	linear	PAT 31-AUG-2001
Sequence 3 from Patent WO0157219.				

AX207820	AX207820
GI:15422467	GI:15422467
AX207820.1	AX207820.1
KEYWORDS	KEYWORDS
VERSION	VERSION
ACCESSION	ACCESSION

SOURCE	ORGANISM
unidentified.	unidentified.
unidentified.	unclassified.

Query Match	10.28;	Score 126.4;	DB 6;	Length 1073;
Best Local Similarity	56.78;	Pred. No. 1.2e-24;		
Matches 254; Conservative	0;	Mismatches 191;	Indels 3;	Gaps 1

OY	338	ctatctcgatcttcctcgacagatbgtgtgtgtctcgtgaatctttaatagcagctc	397
Db	143	CTATTAAATGAATTTGATCATCAGCAAGTGTGGACCTTCAAGGTCAGAAACCTTGTGGCAGTTC	202
OY	398	ctcttagccgagacacttaagcctgtcactcttcatttaataagcctgttagacaagaat	457
Db	203	CACGAAAGTGCACAGTGTGACCCCAAGTCACTGTTGGCTGTATTCACATGCAGATATCCAGAG	262
OY	458	tcaagtgaacaagaaaggtaataatbgttttaacctgtggaatcaaggaaagaatctgtgc	517
Db	263	CTCTTGACCAAGCGCAGAGGGGATCCCATTTATTTGGGATCCAGATCCAGAAATATGTGT	322
OY	518	tctctgtgcagaaatttaagggcaagcctacttttcagcttaagaaaaaatctatcag	577
Db	323	TGTATTGTAGAGAGTTGTGGACACGCCACATTCACACTTAAGAAGCAGAAAGATCATGG	382
OY	578	aacctgaatgtgagagaagaagacacagaagcccttctctcttltccacataaagaagct	637
Db	383	ATCTGTATATGGCCAAACCCGACGCCCGGAAACCTTCTTTTCACCGTGCAGAAAGATGSTA	442
OY	638	ccactctgtcttcttaagtcagtccttaccctcgtgtgtatagcacctccaccacat	697
Db	443	GGACCTCCACACCTTATAGTGTGTGGCTTCCCGCATGTGTATTCCTCTCCACAGA--	499
OY	698	caggacagcccacttcttcaccaaagagagagacataactaactaactaactctact	757
Db	500	GAGACACAGCCATTCATTCTGCACCTTAGAAACTTGGGAAGTACATACAAACACTGCTTTGAAT	559
OY	758	tagattctgttggaataatccacagcctag	785
Db	560	TAAATATTAATGACTGGAACCTCAGCCTAG	587

RESULT 14
AF206696

LOCUS	AF206696	1177 bp	mRNA	linear	PRI 01-NOV-2001
DEFINITION	Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.				

ACCESSION	AF206696
VERSION	AF206696.1
KEYWORDS	GI:11493847
SOURCE	human.

ORGANISM	Homio sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 11)
Debets, R., Timans, J.C., Homey, B., Zurawski, S., Sana, T.R., Lo, S.,
Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and
Wassilak, P.

gene	1. .1177
	/gene="IL1E"
CDS	67. .576

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an IL-1-like receptor IL-1RP2 resulting in IL-1-like
signaling cascade; antagonized by IL-1d"
/codon_start=1
/product="interleukin-1 epsilon"
/protein_id="AAG35670.1"
/db_xref="GI:11493848"
/translation="MRGTGPGADGGRAVYQSMKPTGTINDLNOQVMTLOGONLVA
VPDSVPTVAIVITCKYKPEALBOGRSDPIYLGIONPEMCYCEKVGSDPTLOLKEO
KIMDLGSGPEPVAKPELFYRAKRTGRTSTLESVAFPDMWFLASKRDPPIIITSELGKSN
TAFELIND"
BASE COUNT      320 a      267 g      341 t
ORIGIN

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Query Match	10.2%;	Score 126.4;	DB 9;	Length 1177;
Best Local Similarity	56.7%;	Pred. No. 1.2e-24;		
Matches 254; Conservative	0;	Mismatches 191;	Indels 3;	Gaps 1.

QY	338	ctatccgfatccttcgcagaaatgctgctggtccctgagtgaatcctttaatagcacc	397
Db	143	CTATTAAATGATTGTAATCAGCAAGGTGGACCCCTTCAGGTCAGAACTTGTGGCAGTTTC	202
QY	338	ctcttagccgcgcgaactaaagcctgctaactctcaattataatcctgtagagacaagaat	457
Db	203	CACGAAGTGACAGTGTGACCCGACGACACTGTGTGTATTACATGCAAGTATCCAGAG	262
QY	458	tcagtgacaagaagaagggtataatagtttacctgtggatcaagggaaaagatcctctc	517
Db	263	CTCTTGACCAAGGCGAGAGGGGATCCCATTTATTGTGGAAATCCAGAAATCGTGT	322
QY	518	tctctgtgcagaaattcaaggcaagcctaacttgcagcttaaggaaaaaatatcatg	577
Db	323	TGTAATTGTGAGAGGTGTGGAGACAGCCCACTTCACACTTAAAGCAGAAAGATCATGG	382
QY	578	acctgtatgtgagagaagaagacagaaagcccttctctctttccacaataaagaagct	637
Db	383	ATCTGTATGCGCCAAOCCGAGGCCCGTGAAGAACCCCTTCTTTCACCGTCCCAAGACTGTA	442
QY	638	ccaactctgtcttcacgcagctctcttaacctggtgtgtatagcacctaccacat	697
Db	443	GGACCTCCACCCCTTGAGTCTGTGGCCTTCCCGAGATGCTCATTTCCCTCCCAAGA---	499
QY	698	caggacagcccaactcttccaccagaagagagagatataactataactaactaactctact	757
Db	500	GAGACACAGCCCATCATCTTGTGACTTCAGAACTTGGGAATGCTATACAAACACTGCCTTTGAT	559
QY	758	tagattctgtggaataaattccagccttag	785
Db	560	TAAATATTAATGACTGAACCTCAGCCTAG	587

RESULT	15
E54910	
LOCUS	E54910 1183 bp DNA linear PAT 07-FEB-2001
DEFINITION	Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
ACCESSION	E54910
VERSION	E54910.1 GI:13019313
KEYWORDS	JP 2000032990-A/1.
SOURCE	unidentified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 1183)
AUTHORS	Peter,R.Y.
TITLE	Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
JOURNAL	Patent: JP 2000032990-A 1 02-FEB-2000;
COMMENT	SMITHKLINE BEECHAM CORP OS Unidentified PN JP 2000032990-A/1 PD 02-FEB-2000 PE 14-MAY-1999 JP 1999134172 PR 28-JAN-1997 US 08/790032 PI PETER R YOUNG PC C1N15/09,A61K38/00,A61K39/395,A61K45/00,C07K14/545,C07K16/24,

PC	C12P21/02,	PC
PC	C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53//A61K31/00,	PC
A61K31/00,		
PC	A61K31/00, A61K31/00, C12M5/00, A61K37/02	
CC	Strandedness: Single;	
CC	Topology: Linear;	
FH	Key	Location/Qualifiers
FT	source	1..1183
FT		Location/Qualifiers 'Unidentified'.
FEATURES		
source		
	1..1183	
	Location/Qualifiers	
	/organism="unidentified"	
	/db_xref="taxon:32644"	
BASE COUNT	329 a 249 c 269 g 356 t	
ORIGIN		

Query Match	Similarity	Score	ID	Length
Best Local Similarity	56.7%	126.4	DB 6	1183
Matches	254	Conservative	0	Mismatches 191; Indels 3; Gaps 1;

Search completed: May 13, 2002, 12:10:34
Job time: 43595 sec

Tue May 14 08:26:34 2002

us-09-723-676-1.rge

Page 11


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4080899"
/clone_1ib="N1H.MGC.57"
/tissue_type="gliblastoma"
/lab_host="DH10B (TI phage-resistant)"
/note="organ: brain; Vector: pNNR-IIB (Clontech); Site_1:
SfiI (ggcgcctctgcgcgc); Site_2: pfiI (ggcgcctctgcgc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows:
5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor

```


GAGAGAGAGATTCGAGTGAATTAATTAATCCCCCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

FEATURES
source Location/Qualifiers

CDS

1..1219
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGI:1901829"
/db_xref="taxon:10090"
/clone="2310043N20"
/sex="male"
/tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
78..629
/note="data source:SPRR, source key:Q9UHA5, evidence:ISS homolog to F1L1 ETA putative"
/codon_start=1
/protein_id="BAB26505.1"
/db_xref="GI:12844800"
/translation="MMAPPOSCVHYLPKSIOMEPNHTMHGSSSPNRYHDSO OMWVLTGNTLTAVPASNNVYITSLIACRDTPEFDYKKNLVEIKRNLCECCY EMEKPTDLKEVDIMNLKERRAKAFLEHIGESTSVFSVLYPGWFLAUSIER QTIILHQRGLVNTNFIIESEK"
1199..1204
/note="putative"
polyA_signal
polyA_site
polyA_site
/note="putative"
BASE COUNT 380 a 272 c 217 g 350 t
ORIGIN

Query Match 23.0%; Score 286.6; DB 11; Length 1219;
Best Local Similarity 72.7%; Pred. No. 1.3e-68;
Matches 370; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

321 agcaccacaatcctatgctatcgtgtaattcgcacagatggtgtgctcgtgagtaaa 380
176 ATCTCCAGAAACTACAGGGTTCTACTGCTACACAGATGATGGTGGCTGACAGTAAA 235
381 tcttcttaataagcgtcctcctttagccgcagcattaagcctcctcatttaatagc 440
236 TACTTTAAACGAGCTCTCTCTCTGAGTGAAGGCTGTCATCTTACTTGATGAGC 295
441 ctgtagagacacgaattcagtgacagaagaaggttaataatggtttactcgtggaataa 500
296 ATCTAGAGACACGGAATTCAGAGTGTAAAGAAAGTATATGTTTCCCTGGGAATCAA 355
501 gggaaaagatcctaa 560
356 GAACAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415
561 gggaaaaaataatcctcgtcctctctctctctctctctctctctctctctctctctct 620
416 GGAAGTAGACATGATGAAATTTGTACAAAGAGAGAAACACAAAAAGCCTTCTGTTCTA 475
621 ccaacaataagaagcgtcccaactctctctctctctctctctctctctctctctctctct 680
476 TCAATGGCATAGAGGGCTCCACTTCTGCTTTCAGTCACTCCTCTATCTCTGGTGTAT 535
681 agccaactcacaacatcagcagccatctctcacaagaagagagataactaa 740
536 AGCCACCTCTTCATAGAAAGACAGACATCATCTCTCACATCAGCGGGTAATTTGGT 595
741 taacacaaactctacttagattctgtggaataataacagcctagcgtgtgtgtcgg 800
596 TAACACTTAATCTTACTAGAGTCTGAGAAAGTAATCAACATGGGTATATGTGGCAG 655
801 ttccagatagagatcaagctgtcagag 829
656 CTCGAGGCCACAGAACTCAACTGTTGAAG 684

FEATURES
source

RESULT 3
BM386666/c LOCUS
DEFINITION
UT-R-CNI-cjg-1-09-0-UI-s1 UI-R-CNI Rattus norvegicus cDNA clone
ACCESSION
BM386666
VERSION
BM386666.1 GI:18186719
KEYWORDS
EST.
SOURCE
Norway rat.
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 612)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.iowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized fundus library cDNA library Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 forward
PolyA-Tes.

Location/Qualifiers
1..612
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CNI-cjg-1-09-0-UI"
/clone_lib="UI-R-CNI"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT7n3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CNI
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
bladder, normalized rat cervix, normalized rat brown
adipose, normalized rat fundus, and normalized rat
salivary gland. It was constructed according to the
procedure described by Bonaldo, Lennon & Soares (Genome
Research Genome 6: 791-806, 1996). For construction of
the CNI library, plasmid DNA from the pool of normalized
libraries was electroporated into competent bacteria for
the production of single-stranded circular DNA. This was
then used as a tracer in a subtractive hybridization with
a driver (PCR amplified inserts from a plasmid DNA template
preparation) comprising: a) a pool of about 34,000 clones
from the Rat Urogen Set corresponding to plates R-5-NA-NM
excluding plates R-5-NM and MN. This pool represented 40%
of the final driver population. b) a pool of about 29,000
clones from subtracted libraries CA0 and CA1 corresponding
to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AXZ through
R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,
R-CA0-BKE, R-CA0-BKG-H, R-CA0-BK-K, R-CA0-BKP through
R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through
R-CA1-BDA, R-CA1-BHZ through R-CA1-BUF, R-CA1-BUR,

Source

1. 475
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MGC10527124"
 /clone_11b="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114/9b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was purified with adaptors complementary to the insert adaptors and adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 140 a 87 c 97 g 151 t
 ORIGIN

Query Match 7.3%; Score 90.6; DB 12; Length 475;
 Best Local Similarity 76.6%; Pred. No. 3.4e-14;

Matches 111; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 421 gtcactcttcattatagcctgttagagacagaattcgtgcagaagaaggtat 480

Db 35 CTCATTCTTACCTTGATACATGTAGACAGACAAATTCACAGATTAAGAAAGTAT 94

QY 481 atggtttcccttggaatcaaggaaagatctgtctcttcctgtgcagaatcaggc 540

Db 95 CTAGTTTCTCGAATCAAGAACAAATCTGCTTCGTCTGCTGATGAGAGC 154

QY 541 aagcctacttgcagcttaagaaa 565

Db 155 AAACCACTTGCACCTTAAAGTAA 179

RESULT 6

AM853610 536 bp mRNA linear EST 19-MAY-2000

LOCUS RCI-CT0252-170200-025-c06 CT0252 Homo sapiens cDNA, mRNA sequence.

AM853610

VERSION AM853610.1 GI:7949212

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 536)

Authors: Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

2020263

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

FEATURES

source

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 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?rl=676-RC1-CT0252-170200-025-c06&f3=2000-02-17&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 535.
 Location/Qualifiers

1. 536

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="CT0252"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site: 1; Smat: Site: 2; Smat: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,776 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 140 a 123 c 129 g 144 t
 ORIGIN

Query Match 6.6%; Score 82.2; DB 9; Length 536;
 Best Local Similarity 59.7%; Pred. No. 7.7e-12;

Matches 157; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

QY 523 tctgcagaattcagggcagccctacttgcagcttaaggaaaaataatcagcctg 582

Db 4 TGTGAGAGGTTGGAGAACACCCACATTTGACGATTAAGAACAGATCATGATCTG 63

QY 583 tatgtgagaagaagaagcagccctctctcttcctccacaataagaagctccat 642

Db 64 TATGGGCAACCCGAGCCCGTGAACCTTCTTTCTACCGGCCAAGACTGTAGAGCC 123

QY 643 tctgtcttcaagtcagctcttaccctgtcgtgtcatagaccctccaccatcaga 702

Db 124 TCCACCCCTTGAGTCTGTGGGCTTCCCGGACTGTGATTTG---CTCCACCAAGAGAGAC 180

QY 703 cagcccatcttctccacaagaagagagcctaactaatacctaacttctaactagt 762

Db 181 CAGCCCATCTTCTTGACTTGAAGACTTGGGAAGTCATACACACTGCTTGAATTAAT 240

QY 763 tctgtgataataatccagcctag 785

Db 241 ATTAATGACTGAGACTGAGCCTAG 263

RESULT 7

AM578451/c 559 bp mRNA linear EST 16-MAR-2000

LOCUS RCI-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.

AM578451

VERSION AM578451.1 GI:7253500

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 559)

Authors: Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

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Brazil
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Email: asimpson@ludwig.org.br

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics

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Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=RC1-CT0252-150
600-028-h056t3-2000-06-15&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 555.
High quality sequence stop: 555.

Location/Qualifiers

1. 555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0252"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site:1: Sma1; Site:2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 147 a 131 c 129 g 148 t
ORIGIN

Query Match

Best Local Similarity 59.2%; Score 79.6; DB 10; Length 555;
Matches 155; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

QY 524 gtgcagaatcgaaggcaagcctcttcgagcttaagaaataatcagagccgt 583
DB 555 GTGAGAGGTTGGAGAACAGCCCATTTGAGTAAAGACAGAGATGATGCT 496
QY 584 atgtggaagaagaagcagaagccctctctcttcacataaagaagctcact 643
DB 495 ATGGCCACCCGAGCCCGTGAACCTTCTTCTTACCGGCCAAGACTGGTAGACT 436
QY 644 ctgtcttcagtcagctctctacccctgctggttcataagacacccacacatagagac 703
DB 435 CCACCCCTTGAGTGTGGCCCTTCCCGACCTGCTCATTCCTCCCAAGA---GAGACC 379
QY 704 agccacatcttctaccaaagaagagcacaataaactaacttctactagatt 763
DB 378 AGCCCATCATTTGACTTCAGAACTTGGGAAGTCATACACACTGCTTGAATTAATA 319
QY 764 ctgtggaataatccagcctag 785
DB 318 TAAATGACTGACTGAGCTGAGCTG 297

RESULT 12

AM361164/c 436 bp mRNA linear EST 04-FEB-2000
LOCUS
DEFINITION R01-CT0251-141099-012-C02 CT0251 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM361164
VERSION AM361164.1 GI:6865814
KEYWORDS
SOURCE
ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

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Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0251-
141099-012-c02&t3=1999-10-14&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 436.

Location/Qualifiers

1. 436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site:1: Sma1; Site:2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 123 a 96 c 103 g 114 t
ORIGIN

Query Match

Best Local Similarity 58.8%; Score 77.4; DB 9; Length 436;
Matches 154; Conservative 0; Mismatches 106; Indels 3; Gaps 1;

QY 523 tctgcagaatcgaaggcaagcctcttcgagcttaagaaataatcagagccgt 582
DB 433 TGTGAGAGGTTGGAGAACAGCCCATTTGAGTAAAGACAGAGATGATGCTG 374
QY 583 tatgtgagaagaagaagcagaagccctctctcttcacataaagaagctcact 642
DB 373 TATGGCCACCCGAGCCCGTGAACCTTCTTCTTACCGGCCAAGACTGTAAGACC 314
QY 643 tctgtctttagtcagctctctacccctgctggttcataagacacacacatagaga 702
DB 313 TCCACCCCTTGAGTGTGGCCCTTCCCGACCTGCTCATTCCTCCCAAGA---GAGACC 257
QY 703 cagccacatcttctaccaaagaagagcacaataaactaacttctactagatt 762
DB 256 CAGCCCATCATTTGACTTCAGAACTTGGGAAGTCATACACACTGCTTGAATTAAT 197
QY 763 tctgtggaataatccagcctag 785
DB 196 ATAAATGACTGACTGAGCTGAGCTG 174

RESULT 13

BI961215 594 bp mRNA linear EST 22-OCT-2001
LOCUS
DEFINITION MONOI_7.E06.b1_A005 Monocytes (MONOI) Equus caballus CDNA, mRNA
sequence.
ACCESSION BI961215
VERSION BI961215.1 GI:16319418
KEYWORDS
SOURCE
ORGANISM

horse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 594)
AUTHORS Vandemples,M.L., Cordonnier-Pratt,M.-M., Sudman,M.L., Wentzel,V.E.,
Gingie,A.R., Pratt,L.H., and Moore,J.N.
TITLE An EST database from equine (Equus caballus) monocytes
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2002, 23:38:04 ; Search time 66.4 Seconds
(Without alignments)
4601.929 Million cell updates/sec

Title: US-09-723-676-1

Perfect score: 1244
Sequence: 1 ggtgtctccactgctcagtc.....gcatgtcttcttaactctaa 1244

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata2/ina/5A.COMB.seq: *
2: /cgn2_6/prodata2/ina/6A.COMB.seq: *
3: /cgn2_6/prodata2/ina/6A.COMB.seq: *
4: /cgn2_6/prodata2/ina/68.COMB.seq: *
5: /cgn2_6/prodata2/ina/PCPUS.COMB.seq: *
6: /cgn2_6/prodata2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	324.4	26.1	1190	2	US-08-939-300-1
2	251.8	20.2	320	2	US-08-939-300-3
3	126.4	10.2	1183	2	US-08-790-032-1
4	126.4	10.2	1183	3	US-09-069-619-1
5	70.8	5.7	462	3	US-08-798-414-1
6	70.8	5.7	462	4	US-09-131-247-1
7	70.8	5.7	474	4	US-08-476-860-9
8	70.8	5.7	474	2	US-08-910-733-9
9	70.8	5.7	474	2	US-08-910-884-9
10	70.8	5.7	514	1	US-08-284-784-41
11	70.8	5.7	514	2	US-08-854-811-41
12	70.8	5.7	531	2	US-08-809-185-1
13	70.8	5.7	534	3	US-09-000-630C-24
14	70.8	5.7	534	3	US-08-862-730C-24
15	70.8	5.7	534	3	US-08-422-655-1
16	70.8	5.7	579	2	US-08-476-860-12
17	70.8	5.7	579	2	US-08-910-733-12
18	70.8	5.7	579	2	US-08-910-884-12
19	70.8	5.7	602	1	US-08-459-811-1
20	70.8	5.7	602	1	US-08-459-092-1
21	70.8	5.7	602	2	US-08-459-814-1
22	70.8	5.7	602	2	US-08-425-232-1
23	70.8	5.7	603	2	US-08-471-227-2
24	70.8	5.7	603	1	US-08-484-598-1
25	70.8	5.7	603	2	US-08-479-140-1
26	70.8	5.7	603	3	US-08-477-143-1
27	70.8	5.7	717	1	US-08-284-784-40

28	70.8	5.7	717	2	US-08-854-811-40	Sequence 40, Appl
29	69.2	5.6	1710	3	US-09-000-630C-1	Sequence 1, Appl
30	69.2	5.6	1710	3	US-08-862-730C-1	Sequence 1, Appl
31	69	5.5	998	4	US-09-316-081-1	Sequence 1, Appl
32	69	5.5	998	4	US-09-316-081-1	Sequence 3, Appl
33	68.4	5.5	537	3	US-09-000-630C-25	Sequence 25, Appl
34	68.4	5.5	537	3	US-08-862-730C-25	Sequence 25, Appl
35	68.4	5.5	746	4	US-09-013-810-1	Sequence 1, Appl
36	67	5.4	243	4	US-09-013-810-4	Sequence 4, Appl
37	67	5.4	294	4	US-09-013-810-3	Sequence 3, Appl
38	63.4	5.1	7218	1	US-08-232-463-14	Sequence 14, Appl
39	62.8	5.0	534	3	US-09-000-630C-26	Sequence 26, Appl
40	62.8	5.0	534	3	US-08-862-730C-26	Sequence 26, Appl
41	61.4	4.9	537	3	US-09-000-630C-27	Sequence 27, Appl
42	61.4	4.9	537	3	US-08-862-730C-27	Sequence 27, Appl
43	55.6	4.5	475	4	US-09-131-247-3	Sequence 3, Appl
44	55.6	4.5	1167	4	US-09-131-247-15	Sequence 15, Appl
45	55.6	4.5	1170	4	US-09-131-247-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-939-300-1
Sequence 1, Application US/08939300

Patent No. 5945310

GENERAL INFORMATION:

APPLICANT: Young, Peter R.

APPLICANT: James, Ian E.

TITLE OF INVENTION: A No. 5945310el Member of the IL-1

TITLE OF INVENTION: Family, IL-1 Delta

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAIMER & PRESTITA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,300

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,957

FILING DATE: May 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTITA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1190 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-939-300-1

Query Match

Best Local Similarity

26.1%; Score 324.4; DB 2; Length 1190;

96.8%; Pred. No. 1.3e-96;

Matches 331: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 220 taacttctgcttagaaccagctcctcaccacacatctatctgtctcttc 279
    |||||
DB 31 TCACCTCTCCCTTACTTCTCTAGCTCTCTCACACACATCTGATCTATCTGTTCTCTTC 90
QY 280 acaaaagctctgaagacatcatgaaccacaacagggagagcagcaccacatctctgct 339
    |||||
DB 91 ACAAAAGCTCTGAAGACATCATGAAACCAACAAAGGAGGAGCAGACCCAAATCTTATGCT 150
QY 340 attcgtatctctgacagatggtgtggtcctgaatgtaaatctttaagagctcct 399
    |||||
DB 151 ATTGCTATCTTCACACAGATGATGTTGGTCTCGAGTGGAAATCTTAATAGCAGCTCTT 210
QY 400 cttagccgacatlaagcctgtcactctcattcaatagcctgtagagacagaaatc 459
    |||||
DB 211 CTTAGCCGACGATTAAGCCTGTCACTCTTCAATTAAGCCTGTAGACACAGAAATTC 270
QY 460 agtgaagaagaaagggttaataatgttactctgggaatcaagggaaagatctctgctc 519
    |||||
DB 271 AGTGACAAAGAAAGGGTAATATGTTTACCTGGGAATCAAGGAAAGATCTCTCTCTC 330
QY 520 ttctgtcagaatctcagggcaagcctactcttgagcttaag 561
    |||||
DB 331 TTCTGTGACAAATTCAGGGCAACCTTACTTTCAGCTTAAG 372
```

RESULT 2

US-08-939-300-3
Sequence 3, Application US/08939300
Patent No. 5945310

GENERAL INFORMATION:

APPLICANT: Young, Peter R.
APPLICANT: James, Ian E.
APPLICANT: Connor, Janice R.
TITLE OF INVENTION: A No. 5945310e1 Member of the IL-1
TITLE OF INVENTION: Family, IL-1 Delta
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: RATHER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,300

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,957

FILING DATE: May 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-939-300-3

Query Match 20.2%; Score 251.8; DB 2; Length 320;
Best Local Similarity 93.8%; Pred. No. 4.3e-73;
Matches 270; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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QY 220 taacttctgcttagaaccagctcctcaccacacatctatctgtctcttc 279
    |||||
DB 23 TCACCTCTCCCTTACTTCTCTAGCTCTCTCACACACATCTGATCTATCTGTTCTCTTC 82
QY 280 acaaaagctctgaagacatcatgaaccacaacagggagagcagcaccacatctctgct 339
    |||||
DB 83 ACAAAAGCTCTGAAGACATCATGAAACCAACAAAGGAGGAGCAGACCCAAATCTTATGCT 142
QY 340 attcgtatctctgacagatggtgtggtcctgaatgtaaatctttaagagctcct 398
    |||||
DB 143 ATTGCTATCTTCACACAGATGATGTTGGTCTCGAGTGGAAATCTTAATAGCAGCTCTT 202
QY 399 tcttagccgacatlaagcctgtcactctcattcaatagcctgtagagacagaaatc 458
    |||||
DB 203 TCTTAGCCGACGATTAAGCCTGTCACTCTTCAATTAAGCCTGTAGACACAGAAATTC 262
QY 459 cagtgaagaagaaagggttaataatgttactctgggaatcaagggaaagatctctgctc 506
    |||||
DB 263 CAGTGACAAAGAAAGGGTAATATGTTTACCTGGGAATCAAGGAAAGATCTCTCTCTC 310
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RESULT 3

US-08-790-032-1
Sequence 1, Application US/08790032
Patent No. 5863769

GENERAL INFORMATION:

APPLICANT: Young, Peter
APPLICANT: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/790,032

FILING DATE: 28-JAN-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Schreck, Patricia A

REGISTRATION NUMBER: 33,777

REFERENCE/DOCKET NUMBER: ATG50051

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5031

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1183 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-790-032-1


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Query Match Similarity      10.2%; Score 126.4; DB 2; Length 1183;
Best Local Similarity      56.7%; Pred. No. 1.9e-31;
Matches 254; Conservative   0; Mismatches 191; Indels    3; Gaps    1.

QY 338 ctatcgtgattcttcagacagatgctggtgccttgatgtgaatacttctaataagcgtc 397
    ||||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 151 cttatgatgatgttatgcatacgcaaatgttgacccttcagggtcagaacctgttgccagtgc 210

QY 398 ccttaagccgcagcatlaagcctgtgcacttcatttaaiaagcgttagagacaagaat 457
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 211 CACGAAGTCAGCTGTGACCCTCCAGTACTGTGTGTATVCAATGCAGATFTCCAGAGG 270

QY 458 tcaagtacaaagaaaaggttaatatgttttacctgggaatcaaggaaaaagatctctgc 517
    ||||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 271 CTCCTTGAGCAAGGACGAGGGGATFCCCATTTATTGGGAATFCCAGATFCCAGAAATGTGT 330

QY 518 tcctctgtgcagaatlcaggcgaagcctactcttcagcttaagaaaaaataatactg 577
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 TGTATTGTAGAAGGTGTGGAGAACACCACAFTGCGAGCTAAAAGAGCAGAAATATATAG 390

QY 578 acctgattgtgagaagaagaacagaaagcccctctctctttccacataaagaagct 637
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 391 ATCTGATATGCCAACCCGAGCCCGTAACCCCTTCTTTCTACCGTGCACAGACTGTA 450

QY 638 ccactctgtcttcagtcagtccttcaacctgtgctgattcatagccaactcacacat 697
    || || || || || || || || || || || || || || || || || || || ||
Db 451 GGACCTCCACCCCTTGATGCTGTGCTCCCTCCGAGCTGTTCAATGCTCTCCANAA--- 507

QY 698 caggaaagccccattcttcaccaagaagagagagcataactaaataaacactacttact 757
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 GAACACGCCCATCTATTCTGACTTCAGAACTTGGAAAGTCAATCAACACTGCTTTGAAT 567

QY 758 tagattctgtgaaataatccagcctag 785
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 568 TAATAATTAATGACTGACTCACGCTAG 595

RESULT 4
US-09-069-619-1
; Sequence 1, Application US/09069619
; Patent No. 6054559
GENERAL INFORMATION:
APPLICANT: Young, Peter and Lisa Marshall
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA_)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,619
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/007,464; and 08/790,032
FILING DATE: Filed 14-JAN-1998; and 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William, T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50051-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:

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? INFORMATION FOR SEQ ID NO: 1 :
?   SEQUENCE CHARACTERISTICS:
?       LENGTH: 1183 base pairs
?       TYPE: nucleic acid
?       STRADEDNESS: single
?       TOPOLOGY: linear
?   MOLECULE TYPE: cDNA
?   US-09-069-619-1

Query Match      10.2%   Score 126.4 : DB 3: Length 1183;
Best Local Similarity 56.7%; Pred No. 1.9e-31;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1

OY    338 ctatcgtgatacttcagacagatgggtggcttgatgtaaaattctttaagaccgc 397
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     151 CATATTAATGATTTGAATCAGCAAGTGWAGACCCCTTCAGGGTCAGAACTTTGGCAGTTC 210

OY    398 ctcttagccgaagcattaaagcctgtcaactcttcaattaagtacgctgtagaagacaagaat 457
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     211 CACGAAGTGCACAGTGTGACCCTCACAGTCTGCTGTATCATCATGCCAAGTATCCAGAG 270

OY    458 tcagtgacaagaagaaaaggtaatatggtttacctggagaatcaaaggaagaaatcctgtgc 517
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     271 CTCTTAGCAAGGCAGAGGGGATCCCATTTATTGGGAAFTCCAGAAFTCCAGAAATGTGTT 330

OY    518 tctctgtcacgaaatctcaggccaagcctaactttgcagcttgaagaaaaaataataatg 577
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     331 TGTATGTGAGAAGGTTGGAGAAACCCCAATTCGACGTAAAAGAGCAGAAATATGATG 390

OY    578 acctgatgttgagaagaagaagcagaagccccttctcttttccaacaataaagaagct 637
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     391 ATCTGATGTGCCAACCCCGAGCCCGGTAAACCTTCTTCTTACGCTGCCAACAAGCTGTA 450

OY    638 caactctgtcttcagtcagtccttcaacctgtgctggttcatalagcaacctcacaacat 697
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     451 GGACCTCACACCTTGATGTGTGGCTTCCCGAGCATGTTGATGCTCTCCCAAGA--- 507

OY    698 caggaaagccccacttcttcaccaagaagagagagcataactaataaacacttctact 757
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     508 GAACACAGCCCATCTTCTGACTTCAGAACTTGGAAGTATATCAACACTGCTTTGAAT 567

OY    758 tagattctgtgataataatccagcctag 785
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
DB     568 TAATAATAATGACTGACTCAGCCTAG 595

RESULT      5
US-08-798-414-1
: Sequence 1, Application US/08798414
: Patent No. 6096728
: GENERAL INFORMATION:
:   APPLICANT: COLLINS, David S.
:   TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING
:   TITLE OF INVENTION: INFLAMMATORY DISEASES
:   NUMBER OF SEQUENCES: 2
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: AMGEN INC.
:   STREET: 1840 De Havilland Drive
:   CITY: Thousand Oaks
:   STATE: California
:   COUNTRY: US
:   ZIP: 91320-1789
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/798,414
:   FILING DATE: 07-FEB-1997
:   CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,419
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,789
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US (Atty Dkt# A-365B-P)
; FILING DATE: 23-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ZINDRICK, Thomas D.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-365C
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..462
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..13
; OTHER INFORMATION: /note="Initial methionine is
; OTHER INFORMATION: optional."
; US-08-798-414-1

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Query Match          5 7%; Score 70.8; DB 3; Length 462;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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QY 473 aggttaatagtttactcctggaatcaaggaaagatctctctctctgtgcagaa 532
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 accctcatgctctgttcttgggaatccatgaggaagatgctctctgtgcaact 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 ttcaaggcaagcctacttgcagcttaagaaataatcatatgacctgtatgtgaga 592
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 ctggtgatgagacacacacacacacacacacacacacacacacacacacacac 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 593 agaagcacagaagcctctctctctctctctctctctctctctctctctctctc 652
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 gaagcagacagacagacacacacacacacacacacacacacacacacacacac 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 653 agtcaagctcttaccctgtgtgtatagcacacacacacacacacacacacacac 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 agtctgcccgcctgcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 713 ttctcaccaa 722
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 gcctcaccaa 407

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RESULT 6
; US-09-131-247-1
; Sequence 1, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Herhenson, Susan
; APPLICANT: Bevilacqua, Michael P.
; APPLICANT: Collins, David S.
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131

```

```

; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(462)
; OTHER INFORMATION: Initial methionine is optional
; US-09-131-247-1

```

```

Query Match          5 7%; Score 70.8; DB 4; Length 462;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```

```

QY 473 aggttaatagtttactcctggaatcaaggaaagatctctctctctgtgcagaa 532
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 agctcatgctctgttcttgggaatccatgaggaagatgctctctgtgcaact 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 ttcaaggcaagcctacttgcagcttaagaaataatcatatgacctgtatgtgaga 592
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 ctggtgatgagacacacacacacacacacacacacacacacacacacacacac 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 593 agaagcacagaagcctctctctctctctctctctctctctctctctctctctc 652
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 gaagcagacagacagacacacacacacacacacacacacacacacacacacac 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 653 agtcaagctcttaccctgtgtgtatagcacacacacacacacacacacacacac 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 agtctgcccgcctgcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 713 ttctcaccaa 722
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 gcctcaccaa 407

```

```

RESULT 7
; US-08-476-860-9
; Sequence 9, Application US/08476860
; Patent No. 5739282
; GENERAL INFORMATION:
; APPLICANT: COLOTTA, Francesco
; APPLICANT: MUZIO, Maria
; APPLICANT: MANTOVANI, Alberto
; TITLE OF INVENTION: IL-1 ANTAGONIST
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,860
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT MI 94 A 002097
; FILING DATE: 13-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: COLOTTA-1
; TELECOMMUNICATION INFORMATION:

```

```

? TELEPHONE: 202-628-5197
? TELEFAX: 202-737-3528
? TELEEX: 248633
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 474 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? HYPOTHEETICAL: NO
? FEATURE:
? OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G
? OTHER INFORMATION: was added in the first position, for computer program
? OTHER INFORMATION: reason, in order to encode the first amino acid Glu
? OTHER INFORMATION: and further in order to avoid the creation of a stop
? OTHER INFORMATION: codon in the inner region of the sequence
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..468
?
? US-08-476-860-9

```



```

1  APPLICANT:  Roessler, Blake J.
2  TITLE OF INVENTION:  ADENOVIRAL-MEDIATED GENE TRANSFER TO
3  TITLE OF INVENTION:  SYNOVIAL CELLS IN VIVO
4  NUMBER OF SEQUENCES:  2
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE:  CAMPBELL AND FLORES
7  STREET:  4370 La Jolla Village Drive, Suite 700
8  CITY:  San Diego
9  STATE:  California
10 COUNTRY:  United States of America
11 ZIP:  92122
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE:  Floppy disk
15 COMPUTER:  IBM PC compatible
16 OPERATING SYSTEM:  PC-DOS/MS-DOS
17 SOFTWARE:  PatentIn Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER:  US/08/422,655
20 FILING DATE:
21 CLASSIFICATION:  514
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER:  US 08/100,646
24 FILING DATE:  30-JUL-1993
25 ATTORNEY/AGENT INFORMATION:
26 NAME:  Campbell, Cathryn A.
27 REGISTRATION NUMBER:  31,815
28 REFERENCE/DOCKET NUMBER:  P-UM 9693
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE:  (619) 535-9001
31 TELEFAX:  (619) 535-8949
32 INFORMATION FOR SEQ ID NO:  1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH:  543 base pairs
35 TYPE:  nucleic acid
36 STRANDEDNESS:  double
37 TOPOLOGY:  linear
38
39 FEATURE:
40 NAME/KEY:  CDS
41 LOCATION:  1..534
42
43 US-08-422-655-1

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:09:50 ; Search time 23.76 Seconds
(without alignments)
489.457 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNPRKAPKSYAIRDSRQW.....FLTKRGITNNNTFLDSVE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_1101.*
1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT.*
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18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	818	100.0	157	22	AAE04299 Human Interleukin-
2	818	100.0	157	22	AAE04299 Human IL-1 eta. H
3	777	95.0	170	22	AAE05000 Human Interleukin-
4	452	55.3	164	19	AAE02542 Human IL-1 delta P
5	385	47.1	158	21	AAV70217 Human Interleukin-
6	384	46.9	158	21	AAV70218 Human Interleukin-
7	379	46.3	273	22	AAE03417 Human Interleukin-
8	345.5	42.2	169	19	AAE03136 Interleukin-1 rece
9	345.5	42.2	169	20	AAV24043 A human SPOLL-I pr
10	345.5	42.2	169	20	AAV24395 Human Interleukin-
11	345.5	42.2	169	22	AAE06656 Human Interleukin-

12	345.5	42.2	169	22	AAE03008 Human IL-1ra prote
13	345	42.2	130	22	AAE05001 Human Interleukin-
14	344.5	42.1	208	20	AAV24044 Human SPOLL-II P
15	293.5	35.9	160	19	AAE06286 Rodent interleukin
16	293.5	35.9	160	19	AAE06286 Mouse interleukin
17	290	35.5	157	22	AAE06662 A novel polypeptid
18	271.5	33.2	134	21	AAE06924 Human IL-1 recepto
19	271.5	33.2	134	21	AAE06925 Human IL-1 delta P
20	262	32.0	171	19	AAE082543 Primate interleuki
21	234	28.6	218	21	AAE091884 Human IL-1 recepto
22	229	28.0	163	21	AAE097069 Human IL-1 recepto
23	229	28.0	167	21	AAE096932 Human IL-1 recepto
24	229	28.0	176	22	AAE04081 Human extracellular
25	229	28.0	192	21	AAE05297 Human Interleukin-
26	229	28.0	193	21	AAE06934 Processed human IL
27	229	28.0	193	22	AAE07596 Human IL-1 recepto
28	229	28.0	197	21	AAE095300 Human IL-1 recepto
29	229	28.0	198	22	AAE085138 Human IL-1 recepto
30	229	28.0	203	21	AAE096933 Human IL-1 recepto
31	229	28.0	207	21	AAE06938 Human IL-1 recepto
32	229	28.0	218	21	AAE08266 Human IL-1 recepto
33	229	28.0	218	21	AAE06940 Human IL-1 recepto
34	229	28.0	218	21	AAE070927 Human zilla4 prote
35	229	28.0	218	21	AAE070933 Human zilla4-E200K
36	229	28.0	218	21	AAE071084 Human zilla4-E200D
37	229	28.0	218	21	AAE095299 Human Interleukin-
38	229	28.0	218	21	AAE091885 Primate interleukin
39	229	28.0	218	22	AAE085136 Human IL-1 related
40	229	28.0	218	22	AAE047186 IL-1 related polyp
41	227	27.8	218	21	AAE070931 Human zilla4 varia
42	201.5	24.6	155	21	AAE092254 Human IL-1 homolo
43	200.5	24.5	154	22	AAE035263 Interleukin-1L1 re
44	200.5	24.5	155	20	AAE028408 Human Interleukin
45	200.5	24.5	155	22	AAE087601 Human PRO3432. Ho

ALIGNMENTS

RESULT 1	AAE04299	standard; Protein: 157 AA.
ID	AAE04299	
AC	AAE04299;	
XX		
DE	04-SEP-2001 (first entry)	
XX		
XX		Human Interleukin-1 Receptor Antagonist-Like (IL-1ra-L).
XX		
KW	Human; Interleukin-1 Receptor Antagonist-Like; IL-1ra-L; atherosclerosis;	
KW	multiple sclerosis; septic shock; anorexia; psoriasis; osteoporosis;	
KW	emphysema; Alzheimer's disease; gene therapy; transmissible; vulvovaginitis;	
KW	cytostatic; rheumatoid arthritis; autoimmune disease; diabetes; leprosy;	
KW	pulmonary tuberculosis; septicemia; cachexia; hypoglycemia; lung injury;	
KW	Parkinson's disease; eczema; glomerulonephritis; haemorrhage; ischaemia;	
KW	leukaemia; infertility; inflammatory eye disease; acute pancreatitis;	
KW	fibromyalgia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200142305-A1.	
XX		
PD	14-JUN-2001.	
XX		
PF	28-NOV-2000; 2000MO-US24400.	
XX		
PR	10-DEC-1999; 99US-0170052.	
XX		
PA	28-NOV-2000; 2000US-0170052.	
XX		
PI	(AMGE-) AMGEN INC.	
XX		
XX	Welcher AA, Luethy R, Jing S;	

DR WPI: 2001-417857/44.
DR N-PSDB: AAD08531.

PT Novel interleukin-1 receptor antagonist-like polypeptide, its fragment,
PT variant useful for treating multiple sclerosis, septic shock, anorexia,
PT Alzheimer's disease, emphysema, psoriasis, osteoporosis,
PT atherosclerosis -
XX

PS Claim 14; Fig 1; 133pp; English.

CC The present sequence is human Interleukin-1 receptor antagonist-like (IL-
CC 1ra-L) protein encoded by IL-1ra-L cDNA (ATCC Deposit No: PTA-1215). IL-
CC 1ra-L DNA and protein are useful for treating, diagnosing, preventing or
CC ameliorating disorders or conditions involving immune system dysfunction
CC (rheumatoid arthritis, inflammatory arthritides, autoimmune disease,
CC multiple sclerosis, diabetes, transplant rejection), infections (leprosy,
CC viral, bacterial, pulmonary tuberculosis, acute phase response or the
CC liver, septicemia or septic shock), weight disorders (obesity, anorexia,
CC cachexia, hypoglycaemia); neuronal dysfunctions (Alzheimer's disease,
CC Parkinson's disease); lung (acute or chronic lung injury); skin (eczema,
CC psoriasis); kidney (acute and chronic glomerulonephritis); bone
CC (osteoporosis, osteopetrosis); vascular system (hemorrhage, ischaemia,
CC haemorrhagic shock, atherosclerosis, congestive heart failure); tumour
CC cells (leukaemias); reproductive system (infertility); eye (inflammatory
CC eye disease). IL-1ra-L DNA and protein are also useful for treating
CC acute pancreatitis, acute fatigue syndrome or fibromyalgia. IL-1ra-L DNA
CC is useful in gene therapy techniques and chromosome mapping.

XX Sequence 157 AA:

Query Match 100.0%; Score 818; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNPREAARAKSVYAIRDSKQWVWVLSGNSLIAPLSRSIKPTVLIHLACRDTESDKKCN 60
DB 1 mmpgreapaksyairdsqmwvwsqnsliaplsrsikpvtlihlacrdetfsdckegn 60
OY 61 MVLGIGKDKLFCALFCAEIQGKPTQLQKEKNIMDLYVEKKAQKPFLEFHNKKGSTSVFQSV 120
DB 61 mvyigikgdklfcacelqgkptqlqkeknimdyvekkakqpflefnkkgstsvfsgv 120
OY 121 SYPGWFIATSTTSGQPIFLTKERGITNNNTNYLDSVE 157
DB 121 sypgwfiaatsttsgqpifltkergitnntnfyldsve 157

RESULT 2

AAB50444
ID AAB50444 standard; Protein; 157 AA.

XX AAB50444;

XX 13-MAR-2001 (first entry)

XX Human IL-1 etc.

XX Human; IL-1; interleukin-1; IL-1 etc; immunosuppressive;
XX antiinflammatory; antiarthritic; antipsoriatic; inflammation;
XX autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
XX psoriasis.

XX Homo sapiens.

XX MO200071720-A1.

XX 30-NOV-2000.

XX 25-MAY-2000; 2000WO-US14435.

XX 25-MAY-1999; 99US-0135758.
XX 29-OCT-1999; 99US-0162331.

XX (IMV) IMMUNEX CORP.

XX Stims JE, Renshaw BR.

XX WPI: 2001-032039/04.

XX N-PSDB: AAC90487.

PT Novel interleukin-1 eta polypeptides useful as therapeutic agents for
PT treatment of diseases mediated by polypeptide counter-structure
PT molecules and for identifying inhibitors -
XX

PS Claim 4; Page 5; 45pp; English.

CC The present sequence is an interleukin-1 (IL-1) eta polypeptide.
CC The IL-1 eta polypeptide is useful as a therapeutic agent for the
CC treatment of disease mediated by IL-1 eta polypeptide counter-structure
CC molecules and also for identifying proteins associated with IL-1 eta
CC ligands, to screen for potential inhibitors of activity associated with
CC polypeptide counter-structure molecules and in designing inhibitors.
CC It is used to study cellular processes such as immune regulation, cell
CC proliferation, cell death, cell migration, cell-to-cell interaction and
CC inflammatory responses. IL-1 eta promotes inflammatory responses and is
CC involved in the causation and maintenance of inflammatory and/or
CC autoimmune diseases such as rheumatoid arthritis, inflammatory bowel
CC disease, and psoriasis. IL-1 eta polynucleotides can be used to identify
CC IL-1 eta receptors, to study cell signal transduction and the
CC immune system and to identify genes associated with human conditions
CC such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes
CC mellitus, wrinkly skin syndrome, T-cell leukaemia/lymphoma, and tibial
CC muscular dystrophy.

XX Sequence 157 AA:

Query Match 100.0%; Score 818; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNPREAARAKSVYAIRDSKQWVWVLSGNSLIAPLSRSIKPTVLIHLACRDTESDKKCN 60
DB 1 mmpgreapaksyairdsqmwvwsqnsliaplsrsikpvtlihlacrdetfsdckegn 60
OY 61 MVLGIGKDKLFCALFCAEIQGKPTQLQKEKNIMDLYVEKKAQKPFLEFHNKKGSTSVFQSV 120
DB 61 mvyigikgdklfcacelqgkptqlqkeknimdyvekkakqpflefnkkgstsvfsgv 120
OY 121 SYPGWFIATSTTSGQPIFLTKERGITNNNTNYLDSVE 157
DB 121 sypgwfiaatsttsgqpifltkergitnntnfyldsve 157

RESULT 3

AAB85000
ID AAB85000 standard; Protein; 170 AA.

XX AAB85000;

XX 06-AUG-2001 (first entry)

XX Human interleukin-1 receptor antagonist (NOVINTRA B) polypeptide.

XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
XX gonadotropin-like protein; NOVGOV; interleukin-1; NOVINTRA; human;
XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;
XX antiasthmatic; anti allergic.

XX Homo sapiens.

XX MO200140291-A2.

XX 07-JUN-2001.

```

PE 06-DEC-2000; 2000OWO-US33029.
XX
PR 06-DEC-1999; 9905-0169056.
PR 09-DEC-1999; 9905-0169866.
PR 09-DEC-1999; 9905-0169866.
PR 10-DEC-1999; 9905-0170252.
PR 12-JAN-2000; 2000OUS-0175740.
PR 05-DEC-2000; 2000OUS-0170252.
XX
PR (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zerhusen BD;
PI Mezes PS;
XX
XX WPI: 2001-374790/39.
DR N-PSDB; AAF83869.
XX
XX Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
PS Claim 1; Fig 12B; 138pp; English.
XX
XX The invention provides novel polypeptides (NOVX) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVX polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVINTRA B
CC polypeptide.
XX
XX Sequence 170 AA:
SQ
Query Match 95.0%; Score 777; DB 22; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PPSYAIRDSKQWVWLSGNSLIAPLSIRKVTYLAHLACRRTFFSDRKKGMVYLGICG 68
DB 22 PPSYAIRDSRGMVWVLSGNSLIAPLSIRKVTYLAHLACRRTFFSDRKKGMVYLGICG 81
QY 69 KQLCFCAEIQCKPTQLQLEKKNIMPLYEKKAKQKPFLEFHNNEGSTVSQSYSGWEFA 128
DB 82 KQLCFCAEIQCKPTQLQLEKKNIMPLYEKKAKQKPFLEFHNNEGSTVSQSYSGWEFA 141
QY 129 TSTTSGQPIFLTKERGITNNNTNFYLDSE 157
DB 142 TSTTSGQPIFLTKERGITNNNTNFYLDSE 170
RESULT 4
ID AAW82542
XX AAW82542 standard; Protein; 164 AA.
XX
XX AAW82542;
XX
XX 08-FEB-1999 (first entry)
XX
XX Human IL-1 delta protein.
XX

```

[illegible]

```

XX Human Interleukin-1 epsilon protein.
DE
XX Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human.
XX
XX Homo sapiens.
XX
XX WO200011174-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US18771.
XX
XX 21-AUG-1998; 98US-0097413.
XX 31-AUG-1998; 98US-0098595.
XX 11-SEP-1998; 98US-0099974.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Sims JE, Smith DE;
XX
XX WPI: 2000-237653/20.
XX N-PSDB; AA251247.
XX
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to
XX treat inflammatory and immune system-related diseases such as
XX rheumatoid arthritis and inflammatory bowel disease -
XX
XX Claim 1b; Fig 2; 76pp; English.
XX
XX The present sequence is that of human interleukin-1 (IL-1) epsilon
XX protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
XX expressed in spleen, lymph node, thymus, tonsil and leucocyte
XX tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
XX immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
XX activity. It can be used in the treatment of inflammatory or autoimmune
XX diseases such as rheumatoid arthritis, inflammatory bowel disease and
XX psoriasis. The DNA sequence can be used in chromosome identification,
XX gene mapping and study of immune system.
XX
XX Sequence 158 AA:
SQ

```

```

Query Match          47.1%; Score 385; DB 21; Length 158;
Best Local Similarity 49.0%; Pred. No. 7, 1e-35;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

```

```

QY 9 PKSVAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLIACRDTFESDKEKGMVYLIGIG 68
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 10 ppgsaiqdiinhvwlvdqdtllavprkdrmspytlaiscrhvelckdrnplylging 69
QY 69 KDLICFCAEIOGKPTLQLEKKNIMDLYVEKKAQKPFLEFHNKSGSTSVFQSVSPGWFIA 128
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 lnlclmckavgdqptlqkeldmdlynpqpevksflfthysqgrnstfesvaipwfla 129
QY 129 TSTTSGOPIFLTKERGITNNNTNFEYL 153
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 130 vsseggcplllltqelgkanttfdgl 154

```

```

RESULT 6
AAV70218
ID AAV70218 standard; Protein; 158 AA.
XX
AC AAV70218;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon polymorphic variant.

```

```

XX Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; polymorphic variant; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX MISC-difference 12 /note= "Wild type Gln replaced with Arg"
XX
XX WO200011174-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US18771.
XX
XX 21-AUG-1998; 98US-0097413.
XX 31-AUG-1998; 98US-0098595.
XX 11-SEP-1998; 98US-0099974.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Sims JE, Smith DE;
XX
XX WPI: 2000-237653/20.
XX N-PSDB; AA251248.
XX
XX Nucleotide sequences encoding human interleukin -1 epsilon, useful to
XX treat inflammatory and immune system-related diseases such as
XX rheumatoid arthritis and inflammatory bowel disease -
XX
XX Claim 1b; Fig 2; 76pp; English.
XX
XX The present protein sequence is that of human interleukin-1 (IL-1)
XX epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
XX and is mainly expressed in spleen, lymph node, thymus, tonsil and
XX leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
XX immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
XX activity. It can be used in the treatment of inflammatory or autoimmune
XX diseases such as rheumatoid arthritis, inflammatory bowel disease and
XX psoriasis. The DNA sequence can be used in chromosome identification,
XX gene mapping and study of immune system.
XX
XX Sequence 158 AA:
SQ

```

```

Query Match          46.9%; Score 384; DB 21; Length 158;
Best Local Similarity 49.0%; Pred. No. 9, 1e-35;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

```

```

QY 9 PKSVAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLIACRDTFESDKEKGMVYLIGIG 68
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 10 ppgsaiqdiinhvwlvdqdtllavprkdrmspytlaiscrhvelckdrnplylging 69
QY 69 KDLICFCAEIOGKPTLQLEKKNIMDLYVEKKAQKPFLEFHNKSGSTSVFQSVSPGWFIA 128
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 lnlclmckavgdqptlqkeldmdlynpqpevksflfthysqgrnstfesvaipwfla 129
QY 129 TSTTSGOPIFLTKERGITNNNTNFEYL 153
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 130 vsseggcplllltqelgkanttfdgl 154

```

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RESULT 7
AAE03417
ID AAE03417 standard; Protein; 273 AA.
XX
AC AAE03417;
XX
DT 03-AUG-2001 (first entry)
XX

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XX DE Human interleukin-1 receptor antagonist-like (IL-1ra-L).
XX
XX
XX Human, interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
XX rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
XX joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
XX transplant rejection; graft versus host disease; strain; sprain; leprosy;
XX cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
XX clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
XX myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
XX acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
XX eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
XX hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
XX infertility; endometriosis; retinal neuropathy; acute pancreatitis;
XX Kawasaki's disease; cancer.
XX
XX Homo sapiens.
XX
XX MO200141792-A1.
XX
XX 14-JUN-2001.
XX
XX 04-DEC-2000; 2000WO-US32891.
XX
XX 10-DEC-1999; 99US-0170105.
XX
XX 28-NOV-2000; 2000US-0724859.
XX
XX (AMGE-) AMGEN INC.
XX
XX Calzone FJ, Luethy R, Boedighelmer MJ, Zhu J, Chung Y, Jing S;
XX
XX WPI: 2001-381495/40.
XX
XX N-PSDB; AAD06911.
XX
XX
XX Novel interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
XX polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
XX and prevention of diseases such as arthritis, diabetes, transplant
XX rejection
XX
XX Claim 13; Fig 1A; 127pp; English.
XX
XX
XX The present sequence is human interleukin-1 receptor antagonist-like
XX (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or
XX ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
XX which include rheumatoid arthritis, psoriatic arthritis, inflammatory
XX arthritis, osteoarthritis, autoimmune disease, multiple sclerosis, graft
XX lupus, diabetes, transplant rejection, inflammatory joint disease, graft
XX versus host disease and inflammatory conditions resulting from strain,
XX sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
XX immunodeficiency virus (HIV) infection, clostridium-associated
XX diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
XX anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
XX disorder, acute respiratory disease syndrome, cystic fibrosis, asthma,
XX psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
XX Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
XX lymphomas, lung and breast cancer, leukaemia, infertility,
XX endometriosis, retinal degeneration, retinal neuropathy, acute
XX pancreatitis and Kawasaki's disease.
XX
XX
XX Sequence 273 AA:
XX
XX
XX Query Match 46.3%; Score 379; DB 22; Length 273;
XX Best Local Similarity 48.3%; Pred. No. 6.8e-34;
XX Matches 70; Conservative 30; Mismatches 45; Indels 0; Gaps 0;
XX
XX 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLIACRDTESDKRGKMYGICIG 68
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 125 pqrsgtqdlhvwvlgqdlilavprkdrmspytlaliscrvetlekdrqdiylgng 184
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 69 KDLICFCAEIOGKPTLQIKKKKIMDLVYKKAOKPLPFHNKSGSVSVOSVYPCGEIA 128
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 185 lnlcmakvqdpqlclqkexldimlqnpqevkksfilyhsqgsmstiesvafpawfla 244
XX

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```

OY 129 TSTSGOPIELTKERGITNNTFYL 153
DB 245 vssegcpilltqelgkanttldgl 269
XX
XX
XX RESULT 8
XX ID AAM63136 standard; Protein; 169 AA.
XX
XX AAM63136;
XX
XX 14-OCT-1998 (first entry)
XX
XX Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
XX Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
XX IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
XX cancer; anaemia; arthritis; inflammatory bowel disease;
XX graft vs. host rejection; autoimmune; stroke; cardiac ischaemia;
XX acute respiratory disease syndrome; psoriasis; restenosis;
XX traumatic brain injury; acquired immune deficiency syndrome;
XX cachexia.
XX
XX Homo sapiens.
XX
XX EP855404-A1.
XX
XX 29-JUL-1998.
XX
XX 27-JAN-1998; 98EP-0300572.
XX
XX 28-JAN-1997; 97US-0790032.
XX
XX (SMTK ) SMITHKLINE BEECHAM CORP.
XX
XX Young PR.
XX
XX WPI: 1998-389778/34.
XX
XX N-PSDB; AAV42659.
XX
XX
XX New nucleic acid encoding human interleukin-1 receptor antagonist
XX beta polypeptides - and related expression systems, transformed
XX cells, proteins, antibodies, agonists and antagonists, useful for
XX treatment, prevention and diagnosis of inflammation, septicaemia,
XX cancer etc
XX
XX Claim 13; Fig 2; 20pp; English.
XX
XX
XX The present sequence represents human interleukin-1 receptor antagonist
XX beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in
XX inflammatory responses, and are produced as zymogens which are cleaved
XX upon secretion to yield mature carboxyl terminal 17 kd fragments.
XX IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
XX chronic and acute inflammation, septicemia, cancer, anaemia, arthritis,
XX inflammatory bowel disease, graft vs. host rejection, autoimmunity
XX stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
XX psoriasis, restenosis, traumatic brain injury, acquired immune
XX deficiency syndrome (AIDS) and cachexia. These conditions (or
XX susceptibility to them) may be diagnosed by detecting mutations in the
XX IL-1ra-beta coding sequence analysing a sample for presence or amount
XX of IL-1ra-beta.
XX
XX
XX Sequence 169 AA:
XX
XX
XX Query Match 42.2%; Score 345.5; DB 19; Length 169;
XX Best Local Similarity 45.0%; Pred. No. 1.9e-30;
XX Matches 68; Conservative 29; Mismatches 35; Indels 1; Gaps 1;
XX
XX 4 QREAPKSYAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLIACRDTESDKRGKMY 63
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 17 qsmckpiltgltndingqwtlqgqnlvavprsdsvtprvtvavltckypaalqsgvqdp 76
XX

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```

OY 64 LGIKGKDLCLFCALTEQKPTQLQKEKNIMDLVYKKAQKPELFPHNKGSTSVFQSVSY 123
    |||: ::||:| :: :|||:||||: ||||: : ||||: | || :|||:|
DB 77 IgiqnpemclcyckvgeqplqlkqkImdlygqpevpkPflfyraktgtstlesvafp 136
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
OY 124 GWFATSTSGQPIFLTKERGITNTNTNFYLD 154
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 137 dwfiasskrd-qpliltseIgksyntafeln 166
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|

RESULT 9
AAV24043
ID AAV24043 standard; Protein: 169 AA.
XX
AC AAV24043;
XX
DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcaemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
XX Homo sapiens.
OS
XX
XX MO9937662-A1.
PN
XX
XX 29-JUL-1999.
PD
XX
XX 26-JAN-1999; 99WO-US01575.
PE
XX
XX 27-JAN-1998; 98US-0013810.
PR
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
PA
XX
XX Busfield SJ;
PI
XX
XX WPI: 1999-458675/38.
DR
XX
XX N-PSDB: AAX86458.
DR
XX
XX New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
XX Example 1; Fig 4A-B; 126pp; English.
XX
XX The present sequence represents a SPOIL-I protein. SPOIL proteins have
XX homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
XX The SPOIL proteins are used as modulating agents in regulating a variety
XX of cellular processes. The products can be used for treating disorders
XX characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
XX metabolism disorder, a proinflammatory disorder or an immune disorder.
XX They can be used for treating e.g. inflammatory diseases and disorders
XX e.g. inflammation, septic shock, stroke, diabetes, arthritis,
XX intercolitis and pneumonitis, epithelial cell and/or skin diseases and
XX disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
XX and Kaposi's sarcoma and other epithelial cancers including squamous cell
XX carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
XX bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
XX disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
XX fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
XX (e.g. osteolytic bone lesions) and hypercalcaemia. SPOIL molecules and
XX SPOIL modulators are useful for regulation of bone mass (e.g. increase in
XX bone mass and/or inhibit bone loss), management of bone fragility (e.g.
XX decrease bone fragility); and prevention and/or treatment of bone pain,

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CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 20; Length 169;
Best Local Similarity 45.0%; Pred. No. 1,9e-30;
Matches 68; Conservative 29; Mismatches 53; Index 1; Caps 1;

OY 4 QREAPKSVATIRDSROMVVLGNSLIAPLSIKPVTLLHACRPTESDREKGMVY 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 17 qsmckpigtgIndngqvtlqgnlvayprdsavpvtvavltckypaalqgrgdpily 76
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 64 LGIKGKDLCLFCALTEQKPTQLQKEKNIMDLVYKKAQKPELFPHNKGSTSVFQSVSY 123
    |||: ::||:| :: :|||:||||: ||||: : ||||: | || :|||:|
DB 77 IgiqnpemclcyckvgeqplqlkqkImdlygqpevpkPflfyraktgtstlesvafp 136
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
OY 124 GWFATSTSGQPIFLTKERGITNTNTNFYLD 154
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
DB 137 dwfiasskrd-qpliltseIgksyntafeln 166
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|

RESULT 10
AAV24395
ID AAV24395 standard; Protein: 169 AA.
XX
AC AAV24395;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human interleukin-1 receptor antagonist beta.
XX
XX Human: interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
XX chronic inflammation; acute inflammation; arthritis; autoimmunity;
XX inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
XX cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
XX traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
XX allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
XX allergic inflammatory disease; delayed hypersensitivity; vaccine.
XX
XX Homo sapiens.
OS
XX
XX MO9936541-A1.
PN
XX
XX 22-JUL-1999.
PD
XX
XX 14-JAN-1999; 99WO-US00847.
PE
XX
XX 29-APR-1998; 98US-0069619.
PR
XX
XX 14-JAN-1998; 98US-0007464.
PA
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PI
XX
XX Marshall L, Young PR;
XX
XX WPI: 1999-430615/36.
DR
XX
XX N-PSDB: AAX90135.
DR
XX
XX New interleukin-1 receptor antagonist beta, useful for treating
PT inflammation and autoimmune diseases
XX
XX Claim 15; Fig 1; 34pp; English.
XX
XX The present sequence represents human interleukin-1 receptor antagonist
XX beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
XX useful for diagnosing diseases (or susceptibility to diseases) related
XX to the expression or activity of IL-1RA beta, by determining mutations
XX in the IL-1RA beta nucleic acid sequences and/or analysing for the
XX presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
XX are also useful for screening for compounds which affect activity of the
XX protein. These can be used in treatment to inhibit (antagonist) or
XX enhance (agonist) IL-1RA beta activity, in addition to direct

```


CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumors, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1epsilon (IL-1epsilon) protein.

XX Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 22; Length 169;

Best Local Similarity 45.0%; Pred. No. 1.9e-30;

Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 4 QREAPKSYAIRDSROWVWVLSGNSLIAPLSRSIKPVTLLIACRDPFESEKGNMYY 63
 DB 17 gsmckpigtltindngywlvggnlvaypsdsvtptvavltckypaalegqgdpily 76
 QY 64 LGIKGKDLCLFCAEIQGKPTLQLEKKNIMDLVEKKAOKPFLFFHNKSGTSVFQSVSYP 123
 DB 77 LGIQNPMECLYCEKVGEPQLIQKEQKIMDLYGQPEVPKFLFYAKGTGRTSLSSVAF 136
 QY 124 GWFIASTSTSGQPIFLFKERGITNTNTNYLD 154
 DB 137 dwfiasskrd-qpiltsejgksyntafeln 166

RESULT 12

AAB83008

XX AAB83008 standard; protein; 169 AA.

AC AAB83008;

XX 21-JUN-2001 (first entry)

DE Human IL-1ra protein.

XX Human; IL-1ra; interleukin-1 receptor antagonist; antibacterial;
 KW immunosuppressive; antiinflammatory; antiarthritic; nephrotropic;
 KW hepatotropic; virucide; cardiatic; vasotropic; antiidiabetic; cancer;
 KW neuroprotective; osteoprotic; cytostatic; immunomodulator; nocitropic;
 KW cerebroprotective; antidepressant; antiatherosclerotic; infection;
 KW immune disease; autoimmune disease; bone disease; neuronal disease;
 KW cardiovascular disease.

XX Homo sapiens.

XX WOJ00119390-A1.

XX 22-MAR-2001.

XX 28-AUG-2000; 2000WO-TB01192.

XX 14-SEP-1999; 99US-0154010.

XX (PFIZ) PFIZER PROD INC.

XX Liltman BH, Woodworth TLG, Dombroski MA;

XX WPI; 2001-327986/34.

PT Synergistic treatment of interleukin (IL)-mediated diseases, useful for
 PT e.g. septic shock, comprises adjunctively administering IL-1 receptor
 PT antagonist polypeptide and non-steroidal IL-1 processing and release
 PT inhibiting agent -
 XX Disclosure; Page 91; 112pp; English.

XX The present sequence is a human interleukin-1 receptor antagonist
 CC (IL-1ra). The present sequence or its variant may be administered
 CC in combination with a non-steroidal IL-1 processing and release
 CC inhibiting agent for the treatment or prevention of IL-mediated disease
 CC states. The composition is useful for treating inappropriate host
 CC responses to infectious diseases where active infection exists at any
 CC body site, e.g. septic shock, disseminated intravascular coagulation,
 CC and/or adult respiratory distress syndrome, acute or chronic
 CC inflammation due to antigen, antibody and/or complement deposition;
 CC inflammatory conditions including arthritis, cholangitis, colitis,
 CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,
 CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is
 CC also useful for treating immune-based diseases including conditions
 CC involving T cells and/or macrophages e.g. acute and delayed
 CC hypersensitivity, graft rejection, graft-versus-host disease;
 CC autoimmune diseases including Type 1 diabetes mellitus and multiple
 CC sclerosis. The composition may be used for treating bone and cartilage
 CC resorption as well as diseases resulting in excess deposition of
 CC extracellular matrix. Such diseases include osteoporosis, periodontal
 CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis
 CC and keloid formation. It is also useful for treating tumors which
 CC produce IL-1 as an autocrine growth factor and for preventing the
 CC cachexia associated with certain tumors. It may be used for
 CC treating neuronal diseases with an inflammatory component e.g.
 CC Alzheimer's disease, stroke, depression and concussion injury and for
 CC cardiovascular diseases in which recruitment of monocytes into the
 CC subendothelial space plays a role, e.g. the development of
 CC atherosclerotic plaques.

XX Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 22; Length 169;

Best Local Similarity 45.0%; Pred. No. 1.9e-30;

Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 4 QREAPKSYAIRDSROWVWVLSGNSLIAPLSRSIKPVTLLIACRDPFESEKGNMYY 63
 DB 17 gsmckpigtltindngywlvggnlvaypsdsvtptvavltckypaalegqgdpily 76
 QY 64 LGIKGKDLCLFCAEIQGKPTLQLEKKNIMDLVEKKAOKPFLFFHNKSGTSVFQSVSYP 123
 DB 77 LGIQNPMECLYCEKVGEPQLIQKEQKIMDLYGQPEVPKFLFYAKGTGRTSLSSVAF 136
 QY 124 GWFIASTSTSGQPIFLFKERGITNTNTNYLD 154
 DB 137 dwfiasskrd-qpiltsejgksyntafeln 166

RESULT 13

AAB85001

XX AAB85001 standard; protein; 130 AA.

XX AAB85001;

XX 06-AUG-2001 (first entry)

DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.

XX NOVX; transmembrane protein; NOVTRAN; neuromedine peptide; NOVNEUR;
 KW gonadotropin-like protein; NOVGOIN; interleukin-1; NOVINTRA; human;
 KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
 KW antibacterial; cerebroprotective; antiidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic.

XX Homo sapiens.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:10:20 ; Search time 14.4 Seconds

(without alignments)
830.514 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818

Sequence: 1 MNFOREAPKSYAIRDSROM.....FLTKERGITNNTNFYDSVE 157

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	200.5	24.5	155	2	JC7104	interleukin-1 rece
2	195.5	23.9	178	2	A44610	interleukin-1 rece
3	183.5	22.4	178	2	C40956	interleukin-1 rece
4	182	22.2	177	2	A30386	interleukin-1 rece
5	182	22.2	180	2	A39386	interleukin-1 rece
6	178.5	21.8	177	2	A54377	interleukin-1 beta
7	170.5	20.8	266	1	ICB01B	interleukin-1 beta
8	166.5	20.0	266	1	ICB01B	interleukin-1 beta
9	163.5	20.0	269	1	ICB01B	interleukin-1 beta
10	158.5	19.4	267	1	JN0724	interleukin-1 beta
11	158.5	19.4	267	1	S38373	interleukin-1 beta
12	158.5	19.4	268	1	A30584	interleukin-1 beta
13	158	19.3	269	1	I55969	interleukin-1 beta
14	155.5	19.0	214	2	JC5646	interleukin-1 beta
15	88.5	10.8	268	1	A61246	interleukin-1 alph
16	84.5	10.3	268	1	ICB01A	interleukin-1 alph
17	78	9.5	534	2	S56785	TCPI-related prote
18	77.5	9.5	786	2	E86268	hypothetical prote
19	77	9.4	493	2	T19383	hypothetical prote
20	76.5	9.4	270	2	I46620	interleukin-1 alph
21	76.5	9.4	1533	2	F71274	hypothetical prote
22	75.5	9.2	270	1	I50532	interleukin-1 alph
23	75	9.2	520	2	S45753	probable membrane
24	74.5	9.1	386	2	S49218	histidine decarbox
25	74	9.0	269	2	S16671	Dd31 protein - sli
26	74	9.0	932	2	G86857	isolucine-cRNA 1
27	74	9.0	1101	2	T26919	hypothetical prote
28	73.5	9.0	309	2	B86152	hypothetical prote
29	73.5	9.0	376	2	T39056	hypothetical prote

30	73	8.9	585	2	T50325
31	73	8.9	1045	2	B30239
32	72.5	8.9	197	2	T46496
33	72.5	8.9	394	2	D65167
34	72	8.8	268	1	B24073
35	72	8.8	417	1	S20608
36	72	8.8	418	2	I52968
37	71.5	8.7	555	2	B72341
38	71.5	8.7	871	2	S68482
39	71.5	8.7	1058	1	GNEF17
40	71	8.7	270	1	ICMS1
41	71	8.7	454	2	A41659
42	71	8.7	885	2	I38968
43	70.5	8.6	342	2	S76580
44	70.5	8.6	522	2	S75491
45	70.5	8.6	712	2	E81196

ALIGNMENTS

```
RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 21-Jul-2000
C:Accession: JC7104
R:Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A>Title: IL1RH1: A novel interleukin-1 receptor antagonist gene.
A:Reference number: JC7104; M0ID:99443727
A:Accession: JC7104
A:Molecule type: mRNA
A:Residues: 1-155 <MUL>
A:Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C:Genetics:
A:Gene: IL1RH1
A:Map position: 2q14
C:Keywords: macrophage

Query Match          24.5%; Score 200.5; DB 2; Length 155;
Best Local Similarity 35.1%; Pred. No. 1.1e-12;
Matches 54; Conservative 24; Mismatches 61; Indels 15; Gaps 6;

QY 12 VAIRDSROWWVLSGNSLIAPL--SRSIKPYVHLIACR--DTEFSDKEKGNMYIGIK 67
DB 9 FRKKDALKVLYLHNNQLLAGLHAGKVIKGEISVVPNRMIDASTSP-----VILGVQ 62
QY 68 GKDLCFCAEIOGKPTIOLKEKNIMDIYVEKKAOKPFLFHNKSGTSVQSVSPGWEI 127
DB 63 GGSQCLSCG-VGQEPPLTLEPVNIMELYLGAKESSFTFYRDMGLTSSFSAAYPGWFL 121
QY 128 ATSTSGOPFLTK--ERGITNN--TNFYDSVE 157
DB 122 CTYPEADQPVRLQLPENGGMNAPITDFYQOCD 155

RESULT 2
interleukin-1 receptor antagonist precursor - mouse
M:Alternate names: IL-1Ra
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #ext_change 16-Jul-1999
C:Accession: A44610; B40956; A49031; I56106; I52970
R:Matsumura, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A>Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph
A:Reference number: A44610; M0ID:91316273
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
```

Proc. Natl. Acad. Sci. U.S.A. 88, 5237-5236, 1991

A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family
A:Reference number: A40956; MUID:91271363
A:Accession: B40956

A:Molecule type: DNA
A:Residues: 7-178 <EIS>

A:Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R.Shuck, M.E.; Bessalu, T.E.; Tracey, D.E.; Bienkowski, M.T.
Eur. J. Immunol. 21, 2775-2780, 1991

A>Title: Cloning, heterologous expression and characterization of murine interleukin 1
A:Reference number: A49031; MUID:92037824
A:Accession: A49031

A:Molecule type: mRNA
A:Residues: 23-178 <SHU>

A:Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A.Experimental source: peritoneal macrophages, ICR strain
R.Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991

A>Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
A:Reference number: 156106; MUID:91250712
A:Accession: 156106

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-178 <RES>

A:Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R.Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994

A>Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulation
A:Reference number: 152970; MUID:94271931
A:Accession: 152970

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-178 <RE2>

A:Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C:Genetics:

A:Gene: IL-1rn
A:Introns: 40/2; 70/1; 107/3
C:Superfamily: Interleukin-1
C:Keywords: cytokine receptor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 23.9%; Score 195.5; DB 2; Length 178;
Best Local Similarity 33.6%; Pred. No. 4.1e-12;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 GREAAPKSYAIRDSRMVWVLGSGNSLIAPL-SRSIK-----PVTLLIACSDTERS 54
Db 31 KRPCMKQARIMDTNQKTFRLRNQLAGYLQGPNILEKIIMVPIDLH----- 80
QY 55 DKEKGMYVLGIKGRDLCEFAELQGPRTLQLEKNIMDLYVERKAQRPFLEHNKGGST 114
Db 81 -----SVPLGIHGKGLCLSCAKSGDDIKQLLEEVNITDLSKNKEEDKRFFIRSEKGP 134
QY 115 SVFOSVSYPGMFIATSTTGOPFELT 140
Db 135 TSFESACPGMFLCTTLEADRPVSLT 160

RESULT 3
C40956
interleukin-1 receptor antagonist precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C:Accession: C40956
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family;
A:Reference number: A40956; MUID:91271363
A:Accession: C40956

```
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-178 <EITS>  
A:Cross-references: GB:M63101; NID:g9204928; PIDN:AAA41434.1; PID:g204929  
C:Superfamily: Interleukin-1  
C:Keywords: cytokine receptor
```

Query Match 22.4%; Score 183.5; DB 2; length 178;
Best local Similarity 31.9%; Pred No. 6,4e+11,
Matches 45; Conservative 26; Mismatches 35; Indels 15; Gaps 2;

OY 4 QREAPKSYAIRDSRQWVVLSGNSLIA----APSRSIKPYLIHLIACRDTEFSDEKEG 59
 : :: |::|::||::|::|::|::|::|::|::|::|::|::|::|::|:
DB 31 KRCKMKAFRIMDINOKFFLYLNNOILINGYLGGPNTKLBEKTIDWPIDFKN----- 81

OY 60 NMVLTGIKGKLCLEFCALIQCKPTILOLKEKNITMDLYVEKKAKRPFLPFHNKESTSVQS 119
 ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
DB 82 --VFLLGHGKCLCSVKASGDGTCLKOLEVNITTDLNKNEEKRFPIRESGPPTSFEES 139

OY 120 VSPGWFIATSTTSGOPIFLF 140
 ::||||::|::|::|::|::|::|::|::|::|::|::|::|:
DB 140 LACPGWLCTTLLEADHPYSLT 160

RESULT 4
A30368
Interleukin-1 receptor antagonist secreted form precursor - human

C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text change 26-May-2000
C:Accession: A40956; I37894; A30368; S08160; S08159; A37822
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene faml
A:Reference number: A40956; MWID:91271363
A:Accession: A40956

A:Molecule type: DNA
A:Residues: 1-177 <ETIS>
A:Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
R:Lemnard, A.; Gorham, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Shear, D.; Solari
Cytokine 4, 83-89, 1992
A>Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonis
A:Reference number: I37894; MWID:92338323
A:Accession: I37894

A>Status: translated from GB/EMBL/DDBt
A:Molecule type: DNA
A:Residues: 1-177 <LEN>
A:Cross-references: EMBL:X64532; NID:g933798; PIDN:CAA45832.1; PID:g933799
R:Carrier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slighrom
J.G.; Siyu, L.C.; Hardie, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.
Nature 344, 633-638, 1990
A>Title: Purification, cloning, expression and biological characterization of an inte
A:Reference number: A30368; MWID:90220867
A:Accession: A30368

A:Molecule type: mRNA
A:Residues: 1-177 <CAR>
A:Cross-references: GB:X53296; NID:g32578; PIDN:CAG37386.1; PID:g32579
A>Note: parts of this sequence, including the amino end of the mature protein, were c
R:Eisenberg, S.P.; Evans, R.U.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H
Nature 343, 341-346, 1990
A>Title: Primary structure and functional expression from complementary DNA of huma
A:Reference number: S08160; MWID:90136921
A:Accession: S08160

A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-177 <EI2>
A:Cross-references: GB:X52015; NID:g32576; PIDN:CAG36262.1; PID:g32577
R:Hannun, C.H.; Willcox, C.J.; Arend, W.P.; Joslin, F.G.; Driggs, D.J.; Heimdal, P.L.;
Nature 343, 336-340, 1990
A>Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibito
A:Reference number: S08159; MWID:90136920
A:Accession: S08159

i:Molecule type: protein

A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
 R:Bienkowski, M.J.; Bessatsu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde, J. Biol. Chem. 265, 14505-14511, 1990
 A:Title: Purification and characterization of interleukin 1 receptor level antagonist p
 A:Reference number: A37822; MUID:90354444
 A:Accession: A37822
 A:Molecule type: protein
 A:Residues: 26-52;70-77;122-127;170-175 <BIE>
 A:Experimental source: culture medium, PMA-stimulated THP-1 cells
 C:Comment: For an alternative splice form, see PIR:A39386
 C:Genetics:
 A:Gene: GDB: IL1RN
 A:Cross-references: GDB:125897; OMIM:147679
 A:Map position: 2q14.2-q14.2
 A:Introns: 39/2; 69/1; 106/3
 C:Superfamily: Interleukin-1
 C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:16-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
 F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 22.2%; Score 182; DB 2; Length 177;
 Best Local Similarity 27.9%; Pred. No. 8; 9e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;
 Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACRDTEFS 54
 Db 30 RKSCKQAERIDVNOKTFYLRNNQVAGYLOGPNVNEEKIDVPIEPHAL----- 81
 Oy 55 DKEGNMYVLGKGDCLCECAEQGKPTLQLEKKNIMDLVEKKAOKPFLFFHNKEGST 114
 Db 82 -----FLGIHGKMKCLSCVKSGETRQLQLEAVNITDLSNKRKODKRAFIKSDSGPT 133
 Oy 115 SVFQSYSPGWFIASTTSGQPIFLTK--ERGITNNNTFYLDSE 157
 Db 134 TSFESACPGWFLCTAMEADQPVSLTNMPDEGV-VTKFYFQDE 177

RESULT 5
 A39386
 Interleukin-1 receptor antagonist, long intracellular splice form - human
 N:Contains: Interleukin-1 receptor antagonist, short intracellular splice form
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C:Accession: I37893; A39386
 R:Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan J. Exp. Med. 182, 623-628, 1995
 A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
 A:Reference number: I37893; MUID:95355865
 A:Accession: I37893
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1180 <RES>
 A:Cross-references: EMBL:X84348; NID:q1008970; PIDN:CAA59087.1; PID:q1008971
 R:Hashkili, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Biglier, C.F.; Jaffe, G.J.; Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
 A:Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
 A:Reference number: A39386; MUID:91219436
 A:Accession: A39386
 A:Molecule type: mRNA
 A:Residues: 1-3,25-180 <HAS>
 A:Cross-references: GB:M55646; NID:q186291; PIDN:AAA59138.1; PID:q186292
 C:Comment: For an alternative splice form, see PIR:A30368
 C:Genetics:
 A:Gene: GDB: IL1RN
 A:Cross-references: GDB:125897; OMIM:147679
 A:Map position: 2q14.2-q14.2
 C:Superfamily: Interleukin-1
 C:Keywords: alternative splicing; cytokine receptor
 F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
 F:1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form

Query Match 22.2%; Score 182; DB 2; Length 180;
 Best Local Similarity 27.9%; Pred. No. 9; 1e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;

Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACRDTEFS 54
 Db 33 RKSCKQAERIDVNOKTFYLRNNQVAGYLOGPNVNEEKIDVPIEPHAL----- 84
 Oy 55 DKEGNMYVLGKGDCLCECAEQGKPTLQLEKKNIMDLVEKKAOKPFLFFHNKEGST 114
 Db 85 -----FLGIHGKMKCLSCVKSGETRQLQLEAVNITDLSNKRKODKRAFIKSDSGPT 136
 Oy 115 SVFQSYSPGWFIASTTSGQPIFLTK--ERGITNNNTFYLDSE 157
 Db 137 TSFESACPGWFLCTAMEADQPVSLTNMPDEGV-VTKFYFQDE 180

RESULT 6
 A54377
 Interleukin-1 receptor antagonist secreted form precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C:Accession: A54377; I46729
 R:Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M J. Biol. Chem. 269, 6962-6971, 1994
 A:Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch
 A:Reference number: A54377; MUID:94165101
 A:Accession: A54377
 A:Molecule type: mRNA
 A:Residues: 1-177 <COM>
 A:Cross-references: GB:S68977; NID:9545740; PIDN:AAB30093.1; PID:9545741
 A:Experimental source: colon tissue
 A:Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBI:P:144169)
 R:Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma Immunology 77, 235-244, 1992
 A:Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. P
 A:Reference number: I46729; MUID:93052512
 A:Accession: I46729
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-177 <GOT>
 A:Cross-references: GB:D21832; NID:9425787; PIDN:BA04860.1; PID:94252205
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine receptor; extracellular protein; glycoprotein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.8%; Score 178.5; DB 2; Length 177;
 Best Local Similarity 31.2%; Pred. No. 2e-10;
 Matches 45; Conservative 21; Mismatches 57; Indels 21; Gaps 2;
 Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACRDTEFS 56
 Db 30 KRCCKQAERIDVNOKTFYLRNNQVAGYLOGPNVNEEKIDVPIEPHAL----- 76
 Oy 57 EKGNNMYVLGKGDCLCECAEQGKPTLQLEKKNIMDLVEKKAOKPFLFFHNKEGSTV 116
 Db 77 -EPQLFLGIQGRKCLSCVKSGETRQLQLEAVNITDLSNKRKODKRAFIKSDSGPTT 135
 Oy 117 FQSYSPGWFIASTTSGQPIFLTK 140
 Db 136 FESASCPGWFLCTAMEADQPVSLTNMPDEGV-VTKFYFQDE 159

RESULT 7
 ICB01B
 Interleukin-1 beta precursor - bovine
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C:Accession: J10010; S01380

R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988
 A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin 1-beta.
 A:Reference number: A94695; MUID:88318652
 A:Accession: J00010
 A:Molecule type: mRNA
 A:Residues: 1-266 <MAL>
 A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
 A:Leong, S.R.; Flagg, G.M.; Lamm, M.; Gray, P.W.
 Nucleic Acids Res. 16, 9054, 1988
 A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
 A:Reference number: S01380; MUID:89016591
 A:Accession: S01380
 A:Molecule type: mRNA
 A:Residues: 1-251, 'A', 253-266 <LEO>
 A:Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
 A:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in vivo form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
 C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 20.8%; Score 170.5; DB 1; Length 266;
 Best Local Similarity 31.4%; Pred. No. 2e-09;
 Matches 48; Conservative 33; Mismatches 51; Indels 21; Gaps 5;

OY 14 IRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIA---CRDIEF-----SDKEKGM--VY 63
 DB 123 LQDRQKSLVLSPCVILKA-----LHLISQEMNREVFCMFQGEERDKKIPVA 172
 OY 64 LGIKGKDLCLFCAEIQGKPTLQKEKNIMDLVEYKAKQKPFLEFHNKGSVSQSVQSYSP 123
 DB 173 LGIKKKNLTLSCVKKGDPTLQLEVD-PKVIYPRNNEKRFYKTEIKNTVEESVLYP 231
 OY 124 GWFATSTSGOPIFLTKERGITNTNFYIDSV 156
 DB 232 NWYISTQIEERPVFLGHRGCGDITDFRMETL 264

RESULT 8
 S23010
 Interleukin-1 beta precursor - sheep
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 08-Jun-1994 #sequence-revision 22-Nov-1996 #text-change 15-Oct-1999
 R:Accession: S23010; S43047; S13092; B61246
 R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
 DNA Seq. 1, 423-426, 1991
 A:Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
 A:Reference number: S23010; MUID:92119335
 A:Accession: S23010
 A:Molecule type: mRNA
 A:Residues: 1-266 <SED>
 A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
 A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addi
 R:Sargan, D.R.
 Submitted to the EMBL Data Library, May 1992
 A:Reference number: S43047
 A:Accession: S43047
 A:Molecule type: mRNA
 A:Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'U', 146-266 <SAR>
 A:Cross-references: EMBL:X54796; NID:g1273; PID:CAA8556.1; PID:g1274
 R:Flisterstrand, C.; Sargan, D.
 Nucleic Acids Res. 18, 7165, 1990
 A:Title: Nucleotide sequence of ovine interleukin-1 beta.
 A:Reference number: S13092; MUID:91088326
 A:Accession: S13092
 A:Molecule type: mRNA
 A:Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'U', 146-266 <FIS>
 A:Cross-references: EMBL:X54796

A:Note: the authors translated the codon AGT for residue 62 as Arg
 R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A:Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A:Reference number: A61246; MUID:92120716
 A:Accession: B61246
 A:Molecule type: mRNA
 A:Residues: 1-144, 'U', 146-266 <AND>
 C:Comment: This protein lacks a conventional signal sequence for protein export. Clea
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
 C:Genetics:
 A:Gene: IL-1-beta
 C:Superfamily: interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 20.4%; Score 166.5; DB 1; Length 266;
 Best Local Similarity 29.2%; Pred. No. 5.1e-09;
 Matches 42; Conservative 38; Mismatches 61; Indels 3; Gaps 3;

OY 14 IRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACRD-TEFSDKEKNVYLGIKGDLC 72
 DB 123 LQDRQKSLVLSPCVILKA-LHLSQEMNREVFCMFQGEERDKKIPVALGIRDKNLY 181
 OY 73 LQCAEIQGKPTLQKEKNIMDLVEYKAKQKPFLEFHNKGSVSQSVQSYSPGFIATSTT 132
 DB 182 LSCVKKKGDPTLQLEVD-PKVIYPRNNEKRFYKTEIKNTVEESVLYPMWYSTSQI 240
 OY 133 SGQPIFLTKERGITNTNFYIDSV 156
 DB 241 EKKPVFLGHRGCGDITDFRMETL 264

RESULT 9
 ICHUIB
 Interleukin-1 beta precursor [validated] - human
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Homo sapiens (man)
 C>Date: 28-Feb-1986 #sequence-revision 15-May-1998 #text-change 15-Sep-2000
 C:Accession: A25542; A29019; A93361; I51852; I65200; I38132; B27616; A01848;
 R:Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
 Nucleic Acids Res. 14, 7897-7914, 1986
 A:Title: Genomic sequence for human proliferin interleukin 1 beta: possible evolution from a
 A:Reference number: A25542; MUID:87040762
 A:Accession: A25542
 A:Molecule type: DNA; mRNA
 A:Residues: 1-5, 'K', 7-269 <CLA>
 A:Cross-references: GB:X04500; NID:g33788
 A:Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
 R:Bensi, G.; Rangel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Meli, M.
 Gene 52, 95-101, 1987
 A:Title: Human interleukin-1 beta gene.
 A:Reference number: A29019; MUID:87248099
 A:Accession: A29019
 A:Molecule type: DNA
 A:Residues: 1-269 <DEN>
 A:Cross-references: GB:M15640; NID:g186281; PIDN:AAA74137.1; PID:g386816
 R:Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Din
 Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
 A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
 A:Reference number: A94023; MUID:85088517
 A:Accession: A94023
 A:Molecule type: mRNA
 A:Residues: 1-5, 'K', 7-269 <AND>
 A:Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
 R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Breed, G.; Price, V.; Gillis,
 Nature 315, 641-647, 1985
 A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complem
 A:Reference number: A93361; MUID:85240547
 A:Accession: A93361
 A:Molecule type: mRNA

[illegible]

10.8%; Score 88.5; DB 1; Length 268;

Search completed: May 10, 2002, 09:12:07
Job time: 107 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:11:00 ; Search time 11.69 Seconds
(without alignments)

492.419 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNFORAPKSYAIRDSROM.....FLTKERGITNTNFIIDSVE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	195.5	23.9	178 1 IL1X_MOUSE	P25085 mus musculus
2	183.5	22.4	178 1 IL1X_RAT	P25086 rattus norv
3	182	22.2	177 1 IL1X_HUMAN	P18510 homo sapien
4	181	22.1	177 1 IL1X_HUMAN	O18999 equus caball
5	178.5	21.8	177 1 IL1X_RABIT	P26890 oryctolagus
6	178	21.8	177 1 IL1X_PIG	O29056 sus scrofa
7	173	21.1	174 1 IL1X_BOVIN	O77482 bos taurus
8	166.5	20.4	266 1 IL1B_SHEEP	P21621 ovis aries
9	164.5	20.1	266 1 IL1B_BOVIN	P09428 bos taurus
10	163.5	20.0	269 1 IL1B_HUMAN	P01584 homo sapien
11	161.5	19.7	267 1 IL1B_FELICA	P41687 felis silve
12	159.5	19.5	266 1 IL1B_CEREL	P51745 cervus elap
13	158.5	19.4	267 1 IL1B_PIG	P26889 sus scrofa
14	158.5	19.4	268 1 IL1B_HORSE	Q28386 equus caball
15	158.5	19.4	268 1 IL1B_MACFA	P79182 macaca fasc
16	158.5	19.4	268 1 IL1B_RABIT	P14628 oryctolagus
17	158.5	19.4	269 1 IL1B_MACMU	P48090 macaca mula
18	158.5	19.4	269 1 IL1B_MACNE	P51493 macaca neme
19	158	19.3	269 1 IL1B_MOUSE	P10749 mus musculu
20	157.5	19.3	266 1 IL1B_CAPHI	P79162 capra hircu
21	157.5	19.3	266 1 IL1B_CERTO	P46648 cercocebus
22	151.5	18.5	269 1 IL1B_RAT	O63264 rattus norv
23	147.5	18.0	268 1 IL1A_CAPHI	P79161 capra hircu
24	147.5	18.0	268 1 IL1A_FELICA	O46613 felis silve
25	87	10.6	268 1 IL1A_SHEEP	O28579 ovis aries
26	85	10.4	268 1 IL1A_BOVIN	P08831 bos taurus
27	84.5	10.3	268 1 IL1A_HORSE	Q28385 equus caball
28	78	9.8	270 1 TCPCG_YEAST	P39077 saccharomyc
29	77	9.4	281 1 EF1D_MOUSE	P57776 mus musculu
30	75.5	9.2	265 1 IL1A_CANFA	O46612 canis famli
31	75.5	9.2	270 1 IL1A_PIG	P18430 sus scrofa
32	75	9.1	520 1 APN2_YEAST	P38207 saccharomyc
33	74.5	9.1	720 1 MK06_RAT	P27704 rattus norv

34	74	9.0	269 1 DD31_DICTDI	Q02465 dictyosteli
35	73	8.9	1045 1 HMD2_YEAST	P12684 saccharomyc
36	72.5	8.9	267 1 IL1A_RABIT	P04822 oryctolagus
37	72.5	8.9	394 1 SENC_ECOLI	P31436 escherichia
38	72	8.8	417 1 HS47_HUMAN	P29043 homo sapien
39	72	8.8	418 1 CBP2_HUMAN	P50454 homo sapien
40	71.5	8.7	426 1 YXCX_ASTLO	P58151 astasia ion
41	71.5	8.7	871 1 SC10_YEAST	Q06245 saccharomyc
42	71.5	8.7	1058 1 POL3_DROME	P04323 drosophila
43	71	8.7	270 1 IL1A_MOUSE	P01582 mus musculu
44	71	8.7	454 1 XYIX_PSEPU	P23099 pseudomonas
45	70.5	8.6	712 1 TBPB_NEIIM	Q9K0V0 neisseria m

ALIGNMENTS

RESULT ID	IL1X_MOUSE	STANDARD:	PRT:	178 AA.
AC	P25085;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)			
DE	(IRAP).			
GN	IL1RN OR IL-1RA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91250712; PubMed=1828262;			
RA	Zahedi K., Seidlin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;			
RT	"Mouse IL-1 receptor antagonist protein. Molecular characterization, gene mapping, and expression of mRNA in vitro and in vivo.";			
RL	J. Immunol. 146:4228-4233(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91316273; PubMed=1830498;			
RA	Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;			
RT	"Cloning and expression of murine interleukin-1 receptor antagonist in macrophages stimulated by colony-stimulating factor 1.";			
RL	Blood 78:616-623(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SWISS;			
RX	MEDLINE=94271931; PubMed=8003626; Prada A.E., Whitehead A.S.;			
RA	Zahedi K.A., Uhlar C.M., Rits M.,			
RT	"The mouse interleukin 1 receptor antagonist protein: gene structure and regulation in vitro.";			
RL	Cytokine 6:1-9(1994).			
RN	[4]			
RP	SEQUENCE OF 7-178 FROM N.A.			
RX	MEDLINE=91271363; PubMed=1828896;			
RA	Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,			
RA	Birancher B.J., Thompson R.C.;			
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: evolution of a cytokine control mechanism.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).			
RN	[5]			
RP	SEQUENCE OF 23-178 FROM N.A.			
RX	MEDLINE=92037824; PubMed=1834470;			
RA	Shuk M.E., Essalu T.E., Tracey D.E., Bienkowski M.J.;			
RT	"Cloning, heterologous expression and characterization of murine interleukin 1 receptor antagonist protein.";			
RL	Eur. J. Immunol. 21:2773-2780(1991).			
CC	-I- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA BELONGS TO THE IL-1 FAMILY.			
CC	-I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			

RT "Primary structure and functional expression from complementary DNA
 of a human interleukin-1 receptor antagonist.";
 RL Nature 343:341-346(1990).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92338323; PubMed=1385987;
 RA Lennard A., Gorman P., Carrier M., Griffiths S., Soctney H.,
 Sheer D., Solari R.;
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 antagonist gene.";
 RL Cytokine 4:83-89(1992).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97146044; PubMed=8992991;
 RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 Arend W.P., Smith M.F., Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 and inducible regulatory regions.";
 RL J. Immunol. 158:748-755(1997).
 RN [16]
 RP SEQUENCE OF 26-45.
 RX MEDLINE=90136920; PubMed=2137200;
 RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J., C.,
 Heimdal P.L., Arnes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 inhibitor.";
 RL Nature 343:336-340(1990).
 RN [17]
 RP SEQUENCE OF 26-52.
 RX MEDLINE=90354444; PubMed=2143761;
 RA Bienkowski M.J., Eessalu T.E., Berger A.E., Trussdell S.E.,
 Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 Heinrichson R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 antagonist proteins from THP-1 cells.";
 RL J. Biol. Chem. 265:14505-14511(1990).
 RN [18]
 RP SEQUENCE FROM N.A. (INTRACELLULAR FORM).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haskell S., Martin G., Van Le L., Morris J., Pearce A., Bigler C.F.,
 Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 receptor antagonist associated with epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 RN [19]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.J., Schall T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 Brunner D.P., Yem A.W., Delbel M.R., Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor
 antagonist protein determined by heteronuclear three-dimensional NMR
 spectroscopy.";
 RL Biochemistry 31:5237-5244(1992).
 RN [110]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306;
 RA Stockman B.J., Schall T.A., Strakalaitis N.A., Brunner D.P.,
 Yem A.W., Delbel M.R., Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 protein.";
 RL FEBS Lett. 349:79-83(1994).
 RN [111]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94320368; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,

RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 resolution.";
 RL J. Biol. Chem. 269:12874-12879(1994).
 RN [112]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 Akesson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 Presence of a disulfide link and a cis-proline.";
 RL Eur. J. Biochem. 227:838-847(1995).
 RN [113]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
 FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING.
 CC -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
 PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -1- DATABASE: NAME=Rad Systems' cytokine source book;
 WWW="http://www.rndsystems.com/cyl_cat/illra.html".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55646; AAA59138.1; -
 DR EMBL: M63099; AAA41943.1; -
 DR EMBL: X52015; CA36262.1; -
 DR EMBL: X53296; CA37386.1; -
 DR EMBL: X64532; CAA45832.1; -
 DR EMBL: U65590; AAB92268.1; -
 DR EMBL: U65590; AAB92270.1; -
 DR PIR: A30368; A30368.
 DR PIR: A37822; A37822.
 DR PIR: S08160; S08160.
 DR PIR: S08159; S08159.
 DR PIR: A40956; A40956.
 DR PIR: A39386; A39386.
 DR PDB: 1ITN; 30-APR-94.
 DR PDB: 2IRT; 15-OCT-94.
 DR PDB: 1IRP; 27-FEB-95.
 DR PDB: 1ILR; 07-FEB-95.
 DR PDB: 1ILR; 01-APR-95.
 DR PDB: 1IRA; 17-JUN-98.
 DR Aarhus/Chent-2DPAGE; 7104; IEF.
 DR Aarhus/Chent-2DPAGE; 7105; IEF.
 DR MIM: 147679; -
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal; Alternative splicing; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 1 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT PROTEIN.
 FT DISULFID 91 141
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR EMBL: M57526; AAA31374.1; -
 DR EMBL: D21832; BAA04860.1; -
 DR PIR: A54377; A54377.
 DR HSSP: P18510; IIR.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PRO0264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 177
 FT DISULFID 91 141
 FT CARBOHYD 109 109
 FT SEQUENCE 177 AA; 20214 MW; F5BC087F097FEFAF CRC64;
 SQ
 Query Match 21.8%; Score 178.5; DB 1; Length 177;
 Best Local Similarity 31.2%; Pred. No. 2.4e-10;
 Matches 45; Conservative 21; Mismatches 57; Indels 21; Gaps 2;
 Oy 4 QREAPKSAIADSRQMWVLSGNSLI-----APLSIKPVTLLIACRDTFS 56
 Db 30 KRPCMQAIRIWDVNOKTFYLRNNQVAGYLOGPNKLEERIDVPL----- 76
 Oy 57 EKGNNVYLGIKGDLCFCFAEIQGKPTLOLEKINIMLYEKKAKQKPFLEPHNKGSTV 116
 Db 77 -EPOLLFLGIGKGLCLSCVKSQDKMKLHLEAVNITDLGNKKDKRFTLRSDSGPTT 135
 Oy 117 FQSVSYPGWFIATSTSGPIFLTK 140
 Db 136 FESASCPGWFLCTALEADQPVGLTTPKAAVKYTKFY 172
 RESULT 6
 IL1X_PIG ID IL1X_PIG STANDARD; PRT; 177 AA.
 AC Q29056;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN) (IRAP).
 GN IL1RN OR IRAP1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_Taxid=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CROSSBREED; TISSUE=Lung;
 RA Yin J., Murtough M.P.;
 RT "Characterization of IRAP in morphine treated pig."
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC -----
 CC EMBL: L3849; AAA9424.1; -
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PRO0264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.

KW Glycoprotein; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 177
 FT DISULFID 91 141
 FT CARBOHYD 109 109
 FT SEQUENCE 177 AA; 20093 MW; 2114DC6119A95F9 CRC64;
 SQ
 Query Match 21.8%; Score 178; DB 1; Length 177;
 Best Local Similarity 29.6%; Pred. No. 2.7e-10;
 Matches 47; Conservative 20; Mismatches 66; Indels 26; Gaps 3;
 Oy 4 QREAPKSAIADSRQMWVLSGNSLIAPLSR-----SIKPVTLIACRDTFS 54
 Db 30 KRPCMQAIRIWDVNOKTFYLRNNQVAGYLOGPNKLEKIDVPEVPH----- 79
 Oy 55 DKEGNNVYLGIKGDLCFCFAEIQGKPTLOLEKINIMLYEKKAKQKPFLEPHNKGST 114
 Db 80 -----FVFLGIHGKGLCLSCVKSQDKMKLQDAVNITDLRNKSEODKRFTRSDSGPT 133
 Oy 115 SVFQSVSYPGWFIATSTSGPIFLTK-ERGITNNNTFY 152
 Db 134 TSFESACPGWFLCTALEADQPVGLTTPKAAVKYTKFY 172
 RESULT 7
 IL1X_BOVIN ID IL1X_BOVIN STANDARD; PRT; 174 AA.
 AC O77482;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN) (IRAP).
 GN IL1RN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 NCBI_Taxid=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98305607; PubMed=9643454;
 RA Kiritawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Ooba Y., Yoshino T., Iwai H.;
 RT "Enzymatic amplification and expression of bovine interleukin-1 receptor antagonist cDNA."
 RL Vet. Immunol. Immunopathol. 62:197-208(1998).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AB005148; BAA31854.1; -
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PRO0264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 174
 FT DISULFID 89 139
 FT CARBOHYD 107 107
 FT SEQUENCE 174 AA; 20093 MW; 2114DC6119A95F9 CRC64;
 SQ
 Query Match 21.8%; Score 178; DB 1; Length 177;
 Best Local Similarity 29.6%; Pred. No. 2.7e-10;
 Matches 47; Conservative 20; Mismatches 66; Indels 26; Gaps 3;
 Oy 4 QREAPKSAIADSRQMWVLSGNSLIAPLSR-----SIKPVTLIACRDTFS 54
 Db 30 KRPCMQAIRIWDVNOKTFYLRNNQVAGYLOGPNKLEKIDVPEVPH----- 79
 Oy 55 DKEGNNVYLGIKGDLCFCFAEIQGKPTLOLEKINIMLYEKKAKQKPFLEPHNKGST 114
 Db 80 -----FVFLGIHGKGLCLSCVKSQDKMKLQDAVNITDLRNKSEODKRFTRSDSGPT 133
 Oy 115 SVFQSVSYPGWFIATSTSGPIFLTK-ERGITNNNTFY 152
 Db 134 TSFESACPGWFLCTALEADQPVGLTTPKAAVKYTKFY 172


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CC      -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC      AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC      -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC      PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC      OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC      SECRETORY PROTEINS.
CC      -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC      -----
CC      CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC      -----
CC      DR EMBL; M35589; AAA30585.1; -.
CC      DR EMBL; X12498; CAA31018.1; -.
CC      DR EMBL; M37211; AAA30584.1; -.
CC      DR PIR; J10010; ICBO1B.
CC      DR PIR; S01380; S01380.
CC      DR HSSP; P01584; H1B.
CC      DR InterPro; IPR002348; IL1_HBGF.
CC      DR InterPro; IPR000975; Interleukin_1.
CC      DR InterPro; IPR003502; Interleukin_1_prop.
CC      DR Pfam; PF00340; IL1; 1.
CC      DR Pfam; PF02394; IL1_propep; 1.
CC      DR PRINTS; PR00262; IL1HBGF.
CC      DR PRINTS; PR00264; INTERLEUKIN1.
CC      DR SMART; SM00125; IL1; 1.
CC      DR PROSITE; PS00253; INTERLEUKIN_1; 1.
CC      KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC      FT PROPEP 1 113
CC      FT CHAIN 114 266 INTERLEUKIN-1 BETA.
CC      FT CONFLICT 252 252 A -> G (IN REF. 2).
CC      SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;
CC
QY      Query Match 20.1%; Score 164.5; DB 1; Length 266;
QY      Best Local Similarity 30.7%; Pred. No. 8.7e-09;
QY      Matches 47; Conservative 33; Mismatches 52; Indels 21; Gaps 5;
QY
QY      14 IRDSQMWVWVLSGNSLIIAPLSRSIKPTVTLIIA---CRDPEF-----SDREKGNM--VY 63
QY      Db 123 LQDRQKSLVLAAPCVLA-----LHLLSQEMNEVEVCFMSFVGGERDKKPIPA 172
QY      64 LGIKGKDCILCAEIOGKPTLQLKKEKNIMDIYVERKAKPFLFFPNKEGSTVPSVSY 123
QY      Db 173 LGIKDKNLYLSCVKKGDPTIQLLEVD-PKYVPRKNMERKRFVFTETIKNTYVEFSVLTP 231
QY      124 GWFATSTTSGOPIFLTKERGITNTNNTNFDLSV 156
QY      Db 232 NWYISTSQIERPVPFLGHFRAGQDITDPRMETL 264
QY
RESULT 10
ID IL1B_HUMAN STANDARD; PRT; 269 AA.
AC P01584;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).
GN IL1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.A.
RX MEDLINE=85088517; PubMed=6083565;
RA Auton P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Dinarello C.A.;

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RL Submitted (XXX-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOTOXIN PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M92060; AAA30814.1; -.
CC HSSP: P01584; 1H1B.
CC InterPro: IPR002348; IL1_HBGF.
CC InterPro: IPR000975; Interleukin_1.
CC InterPro: IPR003502; Interleukin_1-prop.
CC Pfam: PF00340; IL1; 1.
CC Pfam: PF02394; IL1_propep; 1.
CC PRINTS: PR00262; IL1HBGF.
CC PRINTS: PR00125; IL1; 1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
CC CYCLOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC PROPEP 1 115 BY SIMILARITY.
CC CHAIN 116 267 INTERLEUKIN-1 BETA.
CC FT SEQUENCE 267 AA; 30361 MW; 781F9971E32F6AE1 CRC64;
SQ
Query Match 19.7%; Score 161.5; DB 1; Length 267;
Best Local Similarity 31.0%; Pred. No. 1.7e-08;
Matches 49; Conservative 25; Mismatches 59; Indels 25; Gaps 5;
QY 10 KSVATRDSONWVLSGNSLIAPLSRSIKPVTLH-----IACRDEEFDKSGNM 61
DB 121 QYTRFDISQKSLVLSGSEIIRA-----LHLNGQNMNQVVRMSFVHEEENSK 170
QY 62 --VYIGIKGKDCIFCAETIQGKPTTQLEKKNIND--LYVEKKAQKPELFFHNKEGSTSVF 117
DB 171 IYVVICIKKNNLYLSCVMKDKPTQLQLE--MDPKVYPRKKRKEKRVFNKTEIKGVNEF 227
QY 118 QSVSYRGWFIATSTSGQPIFLTKERGITNTNTFYLDV 155
DB 228 ESSQEPNMYISTSQAEEMPEVFLGTRGGDITDFRMETL 265
RESULT 12
IL1B_CERL
ID IL1B_CERL STANDARD; PRT; 266 AA.
AC P51745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]

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RP SEQUENCE FROM N.A.
RA Lookhart E.A.;
RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOTOXIN PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: U20500; AAA62234.1; -.
CC HSSP: P01584; 1H1B.
CC InterPro: IPR002348; IL1_HBGF.
CC InterPro: IPR000975; Interleukin_1.
CC InterPro: IPR003502; Interleukin_1-prop.
CC Pfam: PF00340; IL1; 1.
CC Pfam: PF02394; IL1_propep; 1.
CC PRINTS: PR00262; IL1HBGF.
CC PRINTS: PR00125; IL1; 1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
CC CYCLOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC PROPEP 1 113 BY SIMILARITY.
CC CHAIN 114 266 INTERLEUKIN-1 BETA.
CC FT SEQUENCE 266 AA; 30629 MW; 4F40BAE6FD9F060 CRC64;
SQ
Query Match 19.5%; Score 159.5; DB 1; Length 266;
Best Local Similarity 30.1%; Pred. No. 2.6e-08;
Matches 46; Conservative 33; Mismatches 53; Indels 21; Gaps 5;
QY 14 IRDSQRMWVLSGNSLIAPLSRSIKPVTLHLIA---CRDTEP-----SDKEKGNM--YV 63
DB 123 LQDRQNSLIVLSPCVLKA-----LHLISQMSREVVCMFVQAEEEDNNIPVA 172
QY 64 LGIKGKDCIFCAETIQGKPTTQLEKKNINDLYVEKKAQKPELFFHNKEGSTSVFQSVSY 123
DB 173 LGIRKKNQYLSCKVKKGDTTQLQLEVD--PKVYPRKKRKEKRVFNKTEIKGVNEF 231
QY 124 GWFATSTTSGQPIFLTKERGITNTNTFYLDV 156
DB 232 NWYISTSHPEEKRVFLGHRGGDITDFRMETL 264
RESULT 13
IL1B_PIG
ID IL1B_PIG STANDARD; PRT; 267 AA.
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314975; PubMed=8325511;
RA Huether M.J., Lin G., Smith D.M., Murtough M.P., Molitor T.W.;
RT "Cloning, sequencing and regulation of an mRNA encoding porcine
interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M86725; AAA02584.1; -.
DR PIR; JN0724; JN0724.
DR HSSP; P01584; 1H1B.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1-prop.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PF02394; IL1_propep; 1.
DR PRINTS; PRO0262; IL1HBGF.
DR PRINTS; PRO0264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 114 BY SIMILARITY.
FT CHAIN 115 267 INTERLEUKIN-1 BETA.
SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;
Query Match 19.4%; Score 158.5; DB 1; Length 267;
Best Local Similarity 29.1%; Pred. No. 3.3e-08;
Matches 44; Conservative 28; Mismatches 58; Indels 21; Gaps 4;
QY 14 IRDSQWVWVLSGNSLIAPLSRSIKPVTPLHLA--CRDTEF-----SDKEGKNVY 63
Db 124 LQDKRHKSLVTLGPHMLKA-----LHLTLGDIKREVFMQSMVQGDSDSNKIPVT 173
QY 64 LGIKKCDLFCFAELQKQEPQLQKEKNIMDLVEKKAQKPFLEPHNKGSTVSFQSYSP 123
Db 174 LGIKKKNLYLSCVMNDNFTLQLEDID-PRKRYPRKDEKKEFVETKELKNVEESALYP 232
QY 124 GWFATSTSTSGQPIFLTKRGITNTNTNFYID 154
Db 233 NMYISTSOAEQKPFVFLGNSKGRDITDFTWE 263
RESULT 14
ID IL1B_HORSE STANDARD: PRT; 268 AA.
AC 028386; 077744; 018995;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).

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GN IL1B.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96131982; PubMed=8576682;
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,
Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL Vet. Immunol. Immunopathol. 48:221-231(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285941; PubMed=9622738;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
and determination of their full-length cDNA sequences.";
RL Am. J. Vet. Res. 59:704-711(1998).
RN [3]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=97080493; PubMed=8921838;
RA Kato H., Yoon H.Y., Ohashi T., Watari T., Goitsuka R., Tsujimoto H.,
Hasegawa A.;
RT "Identification of an alternatively spliced transcript of equine
interleukin-1 beta.";
RL Gene 177:11-16(1996).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
(BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D42147; BAA07718.1; -.
DR EMBL; U92481; AAC39256.1; -.
DR EMBL; D42165; BAA22528.1; -.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1-prop.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PRO0262; IL1HBGF.
DR PRINTS; PRO0264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW Alternative splicing.
FT PROPEP 1 115 BY SIMILARITY.
FT CHAIN 116 268 INTERLEUKIN-1 BETA.
FT VARSPPLIC 101 154 MISSING (IN SHORT ISOFORM).
FT CONFLICT 45 45 D -> N (IN REF. 2).
FT CONFLICT 55 55 H -> Q (IN REF. 2).
FT CONFLICT 64 65 AM -> VV (IN REF. 2).

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FT CONFLICT 71 71 V -> M (IN REF. 2).
 FT CONFLICT 110 111 EG -> DD (IN REF. 2).
 FT CONFLICT 118 118 M -> V (IN REF. 2).
 FT CONFLICT 245 245 S -> K (IN REF. 2).
 SO SEQUENCE 268 AA; 30268 MW; 336F27792A1542EA CRC64;

Query Match 19.4%; Score 158.5; DB 1; Length 268;
 Best Local Similarity 30.5%; Pred. No. 3.3e-08;
 Matches 46; Conservative 25; Mismatches 59; Indels 21; Gaps 4;

QY 14 IRDSQMWVWVLSGNSLIAPLSRSIKPVTLLH-----IACRDTFSDEKGNM-VY 63
 DB 125 LRDYHKSLSVLSGACELQA-----VHLNGENTNOQVFCMSFVQGEETDKIPVA 174
 QY 64 LGIKGKDLCLFCAEIQGKPTLQKEKNIMDIYERKAOKPFLFFHNKSGTSVFSQSY 123
 DB 175 LGLKRNLYLSCGMKDGKPTLQLETVD-PNTPKRMKREKRVFNKMEIKGNVEESAMP 233
 QY 124 GWFIATSTTSGQPIFLTKERGITNNNTFYLD 154
 DB 234 NWYISTSOAKSPVFLGNTRGRDITDFTIME 264

RESULT 15
 IL1B_MACFA STANDARD; PRT; 268 AA.

AC P79182;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS Macaca fascicularis (Cub eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCB1_TaxID=9541;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.

CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

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 CC or send an email to license@sib-sib.ch).

CC EMBL: D63353; BAA09677.1; -
 CC HSSP: P01584; 1HTB.
 CC InterPro: IPR002348; IL1_HBGF.
 CC InterPro: IPR000975; Interleukin_1.
 CC InterPro: IPR003502; Interleukin_1_prop.
 CC Pfam: PF00340; IL1; 1.
 CC Pfam: PF02394; IL1_propep; 1.

DR PRINTS: PR00262; IL1HBGF.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 116 BY SIMILARITY.
 FT CHAIN 117 268 INTERLEUKIN-1 BETA.
 SO SEQUENCE 268 AA; 30425 MW; CFB7266E3E2C05B4 CRC64;

Query Match 19.4%; Score 158.5; DB 1; Length 268;
 Best Local Similarity 32.5%; Pred. No. 3.3e-08;
 Matches 51; Conservative 23; Mismatches 54; Indels 29; Gaps 6;

QY 14 IRDSQMWVWVLSGNSLIAPLSRSIKPVTLLH-----IACRDTFSDEKGNM-VY 62
 DB 126 LRDQQLKSLVMSGYPYELKA-----LHLQG-QDLQOQVFSMSFVQGEESNDKIPV 174
 QY 63 YLGKGDLCCLFCAEIQGKPTLQKE---KNIMDIYERKAOKPFLFFHNKSGTSVFS 119
 DB 175 ALGLKAKNLYLSCVAKDKDKPTQLQLESYDPKN---YPRKKMKRFFVFNKIEINNKLEFES 230
 QY 120 VSYGWTATSTTSGQPIFLTKERGITNNNTFYLD 156
 DB 231 AQFPNWIYSTQAESMPVFLGTRGQDITDFTMOFV 267

Search completed: May 10, 2002, 09:12:56
 Job time: 116 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:10:45 ; Search time 24.55 Seconds

(without alignments)
935.428 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNQREAPKSYAIRDSRQW.....FLTKERGITNTNTFYLDSE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	818	100.0	157	4 Q9UHA5	Q9UHA5 homo sapien
2	516	63.1	183	11 Q9D6Z6	Q9D6Z6 mus musculu
3	452	55.3	164	4 Q9NZH7	Q9NZH7 homo sapien
4	385	47.1	158	4 Q9UHA7	Q9UHA7 homo sapien
5	345.5	42.2	169	4 Q9NZH8	Q9NZH8 homo sapien
6	293.5	35.9	160	11 Q9J1A2	Q9J1A2 mus musculu
7	229	28.0	192	4 Q9UHA6	Q9UHA6 homo sapien
8	229	28.0	218	4 Q9NZH6	Q9NZH6 homo sapien
9	229	28.0	218	4 Q9HBF3	Q9HBF3 homo sapien
10	200.5	24.5	155	4 Q9UBH0	Q9UBH0 homo sapien
11	198.5	24.3	155	11 Q9QYU1	Q9QYU1 mus musculu
12	198.5	24.3	156	11 Q9J1G2	Q9J1G2 mus musculu
13	195.5	23.9	159	11 Q70207	Q70207 mus musculu
14	182.5	22.3	178	4 Q9HBF2	Q9HBF2 homo sapien
15	182	22.2	180	4 Q14628	Q14628 homo sapien
16	181	22.1	143	4 Q9UPC0	Q9UPC0 homo sapien
17	176.5	21.6	176	6 Q9BEH0	Q9BEH0 canis famill
18	176	21.5	144	4 Q9BYX1	Q9BYX1 homo sapien
19	172	21.0	177	6 Q9GMZ4	Q9GMZ4 tursiops tr

20	166.5	20.4	176	6 Q9GKK2	Q9GKK2 canis famill
21	163.5	20.0	153	4 Q43645	Q43645 homo sapien
22	158.5	19.4	267	6 Q29082	Q29082 sus scrofa
23	154.5	18.9	266	11 Q9WVG1	Q9WVG1 cavia porcea
24	153.5	18.8	266	6 Q9TKR1	Q9TKR1 tursiops tr
25	142	17.4	267	13 Q73909	Q73909 gallus gall
26	140.5	17.2	269	6 Q9XS77	Q9XS77 trichosurus
27	130.5	16.0	276	13 Q57398	Q57398 cyprinus ca
28	130.5	16.0	276	13 Q9PW18	Q9PW18 cyprinus ca
29	128.5	15.7	260	13 Q9YGD3	Q9YGD3 oncorhynch
30	127.5	15.6	254	13 Q9PT12	Q9PT12 oncorhynch
31	124	15.2	283	13 Q9PVZ5	Q9PVZ5 xenopus lae
32	111.5	13.6	72	6 Q77771	Q77771 equus caball
33	104.5	12.8	272	13 Q9DDF2	Q9DDF2 cyprinus ca
34	101	12.3	272	13 Q9DDF3	Q9DDF3 cyprinus ca
35	83	10.1	118	6 Q9TSJ0	Q9TSJ0 equus caball
36	83	10.1	265	6 Q9TRK2	Q9TRK2 tursiops tr
37	80.5	9.8	547	5 Q9V117	Q9V117 drosophila
38	78.5	9.6	439	10 Q9FJV1	Q9FJV1 arabidopsis
39	77.5	9.5	786	10 Q9FZ71	Q9FZ71 arabidopsis
40	77.5	9.5	3529	5 Q9GP30	Q9GP30 theileria p
41	77	9.4	257	11 Q9CYJ5	Q9CYJ5 mus musculu
42	77	9.4	281	11 Q9CWM2	Q9CWM2 mus musculu
43	76.5	9.4	493	5 Q09479	Q09479 caenorhabd
44	76.5	9.4	1533	2 Q83826	Q83826 treponema p
45	76	9.3	880	11 P97693	P97693 rattus norv

ALIGNMENTS

RESULT 1
ID Q9UHA5 PRELIMINARY: PRT: 157 AA.
AC Q9UHA5:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FILL EYA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RT Sims J.E.,
RT "Four New Members Expand the IL-1 Superfamily.";
RT J. Biol. Chem. 275:1169-1175(2000).
DR EMBL: AF201833; AAF25213.1; -.
DR HSSP: P10749; 2MIB.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1_1.
DR SMART: SM00125; IL1_1.
DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 157 AA: 17702 MW: 7A54F3D7557A3BE3 CRC64;

Query Match 100.0%; Score 818; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.3e-76;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQREAPKSYAIRDSRQWVWVLSGNSLIAAPLSRSIKPYTHLILACRDTFSDKEKN 60
DB 1 MNQREAPKSYAIRDSRQWVWVLSGNSLIAAPLSRSIKPYTHLILACRDTFSDKEKN 60
QY MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKGSIVQSV 120
DB MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKGSIVQSV 120
QY 61 MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKGSIVQSV 120
DB 61 MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKGSIVQSV 120
QY 121 SYPGWFIATSTSGPFLTKERGITNTNTFYLDSE 157
DB 121 SYPGWFIATSTSGPFLTKERGITNTNTFYLDSE 157

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Db 121 SYGMEIATSTSGOPIFLTKERGITNNTNFYLDSE 157
RESULT 2
AC 090626 PRELIMINARY; PRT; 183 AA.
ID 090626
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 2310043N20RIK PROTEIN.
GN 2310043N20RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flaischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seyer T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009787; BAB26505.1;
DR MGI: MGI:1916927; 2310043N20RIK.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRODOM: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.
SO SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;

Query Match 63.1%; Score 516; DB 11; Length 183;
Best Local Similarity 64.2%; Pred. No. 3.6e-45;
Matches 95; Conservative 24; Mismatches 29; Indels 0; Gaps 0;

QY 8 APKSAIDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGNVYLGIG 67
Db 34 SPRNRVHSDQOMVAVLNGTTLTAVPASNKKVYVLSLACRTEFQDVKGNLVFLGIG 93
QY 68 GKDLCECAEIQGKPTQLQKRNIMDLVYEKAKPFLFHNKSGTSVSQSVSGPMFI 127
Db 94 NRNLCEFCVEHEGKPTQLQKRNIMDLVYEKAKPFLFHNKSGTSVSQSVSGPMFI 153
QY 128 ATSTSGOPIFLTKERGITNNTNFYLDSE 155
Db 154 ATSSIERQITLTHQKGLVNTNFYIES 181

RESULT 3
ID 090626 PRELIMINARY; PRT; 164 AA.
AC 090626
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
SO SEQUENCE 164 AA; 16521 MW; FDD2099FAA357A0A CRC64;

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OSTEOBLASTOMA;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL: AF200494; AAF69250.1;
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
SO SEQUENCE 164 AA; 16521 MW; FDD2099FAA357A0A CRC64;

Query Match 55.3%; Score 452; DB 4; Length 164;
Best Local Similarity 94.6%; Pred. No. 1.1e-38;
Matches 88; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNQREAPPSYAIRDSQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGN 60
Db 1 MNQREAPPSYAIRDSQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGN 60
QY 61 MYVLGKDKLCECAEIQGKPTQLQKRNIMDL 93
Db 61 MYVLGKDKLCECAEIQGKPTQLQKRNIMDL 93

RESULT 4
ID 090626 PRELIMINARY; PRT; 158 AA.
AC 090626
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FILI EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Kuchin M., Garza K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL: AF201831; AAF25211.1;
DR HSP: P18510; IL1A.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART: SM00125; IL1; 1.
SO SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 47.1%; Score 385; DB 4; Length 158;
Best Local Similarity 49.0%; Pred. No. 8.1e-32;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY 9 PKSYAIRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGNVYLGIG 68
Db 10 POGSIOIDINHRVWVLODQTLVAVPRKDRSPVITALISCHNVEFLKDRGPIYLGIG 69
QY 69 KDLCECAEIQGKPTQLQKRNIMDLVYEKAKPFLFHNKSGTSVSQSVSGPMFI 128
Db 70 LNLCECAEIQGKPTQLQKRNIMDLVYEKAKPFLFHNKSGTSVSQSVSGPMFI 129

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OY 129 TSTTSGPIFLTKRGITNTNTNFYL 153
 DB 130 VSSEGGCPILITQELGKANTDFGL 154

RESULT 5

Q9NZH8 PRELIMINARY; PRT; 169 AA.

AC Q9NZH8; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.
 RA MEDLINE-20209405; PubMed-10744718;
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of
 the interleukin-1 family";
 RL J. Biol. Chem. 275:10308-10314(2000).

RP SEQUENCE FROM N.A.
 RC TISSUE=PRIMARY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
 RA Debers R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
 RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
 related protein 2; response is antagonized by IL-1d";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF200492; AAF69248.1;
 DR EMBL; AF206696; AAG35670.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Query Match 42.2%; Score 345.5; DB 4; Length 169;
 Best local Similarity 45.0%; Pred. No. 9.8e-28;
 Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

OY 4 QREAPKSYAIRDSRQWVWLSGNSLIAPLSRSIKPYTLHLIACRDFEFSKGNMY 63
 DB 17 QSMCKPITGINDINQWVLOGONLVAVPRSDSVTPVAVATICKYPEALDQGRDDPY 76
 OY 64 LGTIGKGLCFCAELQGPPTQLQKEKNIMDYVEKKAQKPLFFHNKESSTVSFOSVSP 123
 DB 77 LGIONPEKCLCEVGEPTQLQKEQKIMDIYGOPEPVKPLFLYAKTIGRTLSVAPF 136
 OY 124 GWFATSTTSGPIFLTKRGITNTNTNFYL 154
 DB 137 DWFATSSKRD-QPIITLSELGKSYNTAFELN 166

RESULT 6
 Q9JIA2 PRELIMINARY; PRT; 160 AA.

AC Q9JIA2; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1
 SUPERFAMILY 1, EPSILON).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RP SEQUENCE FROM N.A.
 RA MEDLINE-20209405; PubMed-10744718;
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of
 the interleukin-1 family";
 RL J. Biol. Chem. 275:10308-10314(2000).

RP SEQUENCE FROM N.A.
 RA Debers R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
 RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
 related protein 2; response is antagonized by IL-1d";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessl C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AF200493; AAF69249.1;
 DR EMBL; AF206697; AAG35671.1;
 DR EMBL; AK004061; BAB23147.1;
 DR MGD; MGI:1859324; F11.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;

Query Match 35.9%; Score 293.5; DB 11; Length 160;
 Best local Similarity 37.7%; Pred. No. 2e-22;
 Matches 58; Conservative 31; Mismatches 62; Indels 3; Gaps 1;

OY 1 MNPORE--AAPKSYAIRDSRQWVWLSGNSLIAPLSRSIKPYTLHLIACRDFEFSKE 57
 DB 1 MNKEKELRAASPSLRHVODLSRWVLIQNTLTVPRKEQTPVPTITLLPCQYDITLEN 60
 OY 58 KGNMNYLGIGKGLDCLCAELQGPPTQLQKEKNIMDYVEKKAQKPLFFHNKESSTVSF 117
 DB 61 RGDPTYGVOHPMSCLCTCKKGEPVLOLGCNTNEMKNKKEPVKASLFIYHKKSSTISF 120
 OY 118 QSVSPGWFATSTTSGPIFLTKRGITNTNTNF 151
 DB 121 ESAAPGWFIAVCSGSPILITQELGIFITDF 154

RESULT 7
 Q9UHA6 PRELIMINARY; PRT; 192 AA.

AC Q9UHA6; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE FILI ZETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20092888; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garck K.E.,
 RA Sims J.E.;
 RT "Four New Members Expand the IL-1 Superfamily.";
 RL J. Biol. Chem. 275:1169-1175(2000).
 DR EMBL: AF201832; AAF25212.1;
 DR HSP: P18510; 1ITN
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802F612 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 192;
 Best Local Similarity 34.8%; Pred. No. 1e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLACRDTFSDKEKGMNVYIGIKG 68
 DB 31 PKFSIHDOHKVLDVDSGNLIAPDKNYIRPEIFPALA-SLSASAERKSPILLGVSK 89
 OY 69 KDLCLCAEIQGK--PTLQLEKKNIMDLVEKKAQKPFLEFHNKSGTSVFQSVSPGM 125
 DB 90 GECFLYCDKDGQSHPSLQLEKKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 149
 OY 126 FIATSTTSGOPIFLT 140
 DB 150 FICTSCNCPVGV 164

RESULT 8
 ID Q9NZH6 PRELIMINARY; PRT; 218 AA.
 AC Q9NZH6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM A).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
 RX MEDLINE=20209405; PubMed=10744718;
 RA Kumar S., McDonnell P.C., Lohr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of the interleukin-1 family.";
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON CARCINOMA;
 RA Manoj P.P., Mantovani A., Muzio M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
 RA Lewis L., Eigenbrodt C., Henzle W.J., Vandlen R., Filvaroff E.;
 RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1R β .";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF200496; AAF69252.1; -;
 DR EMBL: AF167368; AAG29344.1; -;
 DR EMBL: AF251118; AAG14420.1; -;
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 218 AA; 24138 MW; 96E09310D2CEA68 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
 Best Local Similarity 34.8%; Pred. No. 1.2e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLACRDTFSDKEKGMNVYIGIKG 68
 DB 57 PKFSIHDOHKVLDVDSGNLIAPDKNYIRPEIFPALA-SLSASAERKSPILLGVSK 115
 OY 69 KDLCLCAEIQGK--PTLQLEKKNIMDLVEKKAQKPFLEFHNKSGTSVFQSVSPGM 125
 DB 116 GECFLYCDKDGQSHPSLQLEKKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 175
 OY 126 FIATSTTSGOPIFLT 140
 DB 176 FICTSCNCPVGV 190

RESULT 9
 ID Q9HBF3 PRELIMINARY; PRT; 218 AA.
 AC Q9HBF3;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
 RA Lewis L., Eigenbrodt C., Henzle W.J., Vandlen R., Filvaroff E.;
 RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1R β .";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF251119; AAG14421.1; -;
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
 Best Local Similarity 34.8%; Pred. No. 1.2e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPVTLHLACRDTFSDKEKGMNVYIGIKG 68
 DB 57 PKFSIHDOHKVLDVDSGNLIAPDKNYIRPEIFPALA-SLSASAERKSPILLGVSK 115
 OY 69 KDLCLCAEIQGK--PTLQLEKKNIMDLVEKKAQKPFLEFHNKSGTSVFQSVSPGM 125
 DB 116 GECFLYCDKDGQSHPSLQLEKKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 175
 OY 126 FIATSTTSGOPIFLT 140
 DB 176 FICTSCNCPVGV 190

RESULT 10
 ID Q9UBH0 PRELIMINARY; PRT; 155 AA.
 AC Q9UBH0

GN09B0; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE FILI DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
 DE ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
 GN IL1H1 OR IL1L1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20092888; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
 RA Sims J.E.;
 RT "Four New Members Expand the IL-1 Superfamily.";
 RL J. Biol. Chem. 275:1169-1175(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99443727; PubMed=10512743;
 RA Mulero J.-J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Dirmancic R., Ford J.E.;
 RT "IL1H1: A Novel Interleukin-1 Receptor Antagonist Gene.";
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the
 RT IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Barton J.L., Herbst R., Bosio D., Nicklin M.J.H.;
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the
 RT IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20322477; PubMed=10866108;
 RA Mulero J.J., Nelken S.T., Ford J.E.;
 RT "Organization of the Human Interleukin-1 Receptor Antagonist Gene
 RT IL1H1.";
 RL Immunogenetics 51:425-428(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
 RA Kastalein R.A.;
 RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF201830; AAF25210.1;
 DR EMBL, AF186094; AAF02757.1;
 DR EMBL, AJ242737; CAB59823.1;
 DR EMBL, AJ242738; CAB59823.1;
 DR EMBL, AJ271338; CAB67704.1;
 DR EMBL, AF216693; AAF67981.1;
 DR EMBL, AF230377; AAF91274.1;
 DR HSP, P18510; IL1R.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SMO0125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.
 KM Receptor.
 SQ SEQUENCE 155 AA; 16962 MW; B96DB5BEFA2612E25 CRC64;

Query Match	24.5%;	Score 200.5;	DB 4;	Length 155;
Best Local Similarity	35.1%;	Pred. No. 6.5e-13;		
Matches	54;	Conservative	24;	Mismatches 61; Indels 15; Gaps 6;
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Db      9  FRMDSAIKVLYLHNQNLAGGLHAGKVIKGEISVENRMLDASLSP-----VILGVQ 62
QY      68  GKDLCLFAEIOGKFTLLDLEKKNIMDYVEKKAQPELFFHNKSESTVSPOSVSPGMFI 127
Db      63  GSGQCLISCG-VGOEPTLLLEPYNIMELVGAKESSFTFFRRDMGLTSSFSAAVPMFL 121
QY      128  ATSTTSGGPIFLEK--ERGITNN--TNEVLSDSVE 157
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ID      090Y11      PRELIMINARY;      PRT;      155 AA.
AC      090Y11.
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
GN      IL1HV1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Barton J.L., Nicklin M.J.H.;
RT      "IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed
RL      in Tryptophanblasts and Macrophages."
RL      Submitted (OCT-1999) to the EMBL/Genbank/DBD databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=20209405; PubMed=10744718;
RA      Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA      Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA      Young P.R.;
RT      "Identification and initial characterization of four novel members of
RT      the interleukin-1 family.";
RL      J. Biol. Chem. 275:10308-10314(2000).
DR      EMBL; AJ250429; CAB59831.1; -
DR      EMBL; AF200495; AAF69251.1; -
DR      HSSP; PI8510; IILR.
DR      MGD; MGI:1859325; Il1hv1.
DR      InterPro; IPR000975; Interleukin_1.
DR      Pfam; PF00340; IL1; 1.
DR      SMART; SM00125; IL1; 1.
DR      PROSITE; PS00253; INTERLEUKIN_1; 1.
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[illegible]

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Best Local Similarity	33.6%	Pred. No. 2,2e-12		
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OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX NCBI_TaxID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=FVBKDBA/1 LACJ;				
RX MEDLINE=98209757; PubMed=9550387;				
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;				
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning				
RT and protein expression of intracellular isoform and tissue				
RT distribution of secreted and intracellular IL-1 receptor antagonist in				
RT vivo.";				
RL J. Immunol. 159:5905-5913(1997).				
DR EMBL: AF001795; AAC15251.1; -.				
DR HSSP: P18510; IL1RN.				
DR MGD: MGI:96547; IL1RN.				
DR InterPro: IPR000975; Interleukin_1.				
DR Pfam: PF00340; IL1; 1.				
DR SMART: SM00125; IL1; 1.				
DR PROSITE: PS00253; INTERLEUKIN_1; 1.				
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Db 12 KRPCKMQARIRWDNKTYYLRNNQILAYLOGPNKLEKIDWVIDH----- 61				
OY 55 DKEKNMYVLTGKGDLCFCAEIOGKPTLOLEKKNIMDYEEKKQKPFLEFNKGS 114				
Db 62 -----SVFLGIHGGLCLSCAKSGSDIKQLQLEVVITDLSKNEKEDKRTFIRSEKGP 115				
OY 115 SYFQSVSTPGVFIAITSTTSGPIFLT 140				
Db 116 TSESACPGWFLCTTLEADREVSLT 141				
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AC O9HBF2;				
DT 01-MAR-2001 (TREMBLrel. 16, Created)				
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
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OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA Pan G., Risseer P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,				
RA Lewis L., Eigenbrodt C., Henzle W.J., Vandlen R., Filvaroff E.;				
RT "IL-1h, an interleukin-1-related protein that binds IL-18 receptor/IL-				
RT 1RTP.";				
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AF251120; AAG14422.1; -				
DR InterPro: IPR000975; Interleukin_1.				
DR Pfam: PF00340; IL1; 1.				
DR PRODOM: PD002536; Interleukin_1; 1.				
DR SMART: SM00125; IL1; 1.				
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Best Local Similarity	37.9%	Pred. No. 5,3e-11		
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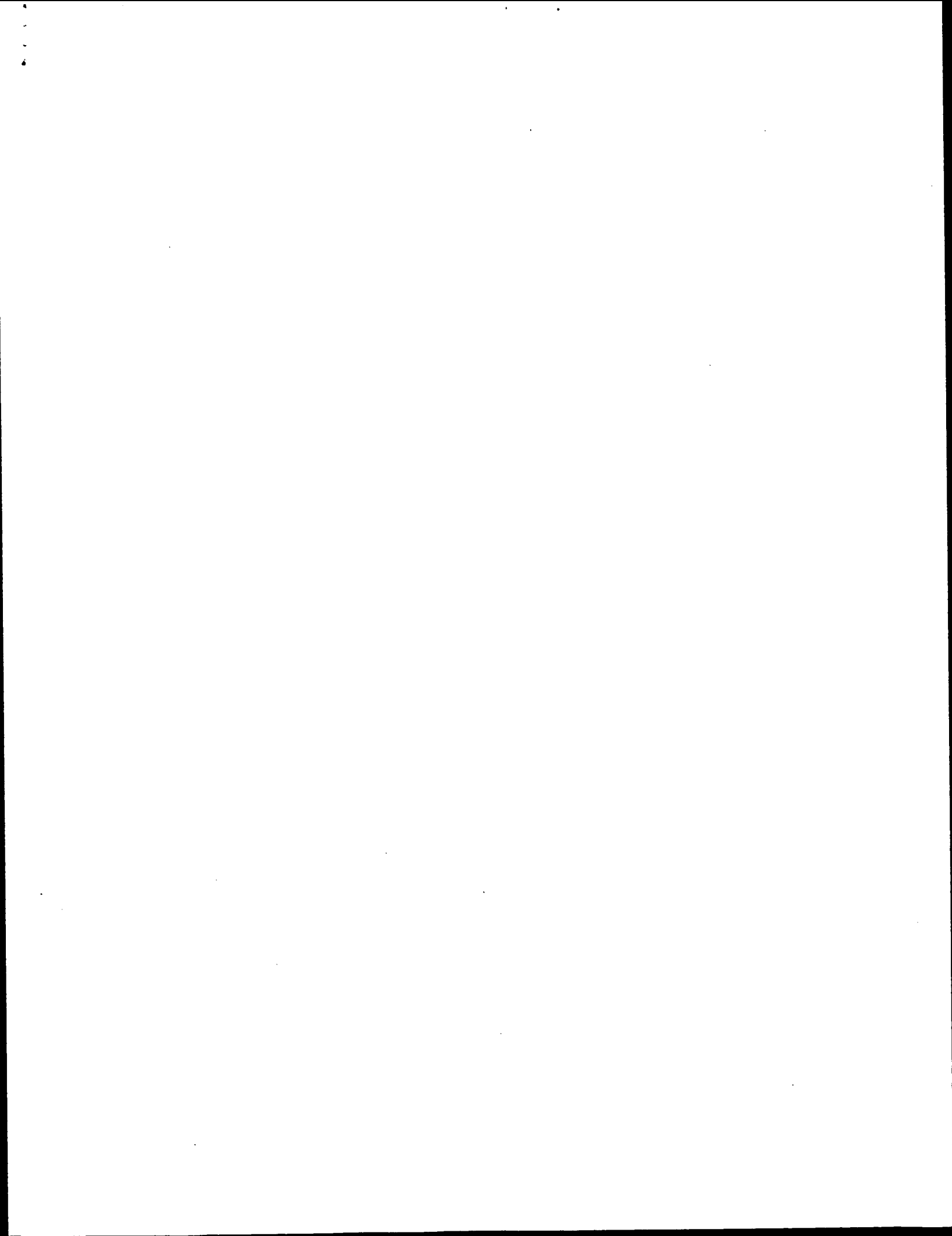
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RESULT 15

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 AC 014628;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
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 GN IL-1RN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95355865; PubMed=7629520;
 RA Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
 RA Introna M., Mantovani A., Colotta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist.";
 RL J. Exp. Med. 182:623-628(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97146044; PubMed=8992991;
 RA Jenkins J.K., Diron R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Arend W.P., Smith M.F., Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions.";
 RL J. Immunol. 158:748-755(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Slightom J.L.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X84348; CAA59087.1; -;
 DR EMBL: U65590; AAB92269.1; -;
 DR HSSP: P18510; IIRP
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
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 QY 55 DKENGMVYLIGIKGDLCEFCAEIOGKPTLOLKEKNIMLYVEKKAKQKPLFFHNKEGST 114
 DB 85 -----FLGIHGKMKLSCVKSQSDETRLQLEAVNITDLSERKQDKRPAFIRSDSGPT 136
 QY 115 SVFQSVSYPCWFPIATSTSGQPIFLT--ERGITNTNTNFIYLDVE 157
 DB 137 TSFESACPCWFLCTAMEADQPVSLTNMDEGVM-VTKFYFQEDE 180



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:09:50 ; Search time 12.56 Seconds
(without alignments)
281.291 Million cell updates/sec

Title: US-09-723-676-2
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Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	452	55.3	164	2	US-08-939-300-2
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3	345.5	42.2	169	3	US-09-069-619-2
4	262	32.0	71	2	US-08-939-300-4
5	200.5	24.5	155	4	US-09-417-455-5
6	195.5	23.9	178	3	US-09-000-630C-21
7	195.5	23.9	178	3	US-08-862-730C-21
8	195.5	23.9	178	4	US-09-417-455-9
9	187	22.9	185	3	US-09-128-155-18
10	186	22.7	153	3	US-08-798-414-2
11	186	22.7	153	4	US-09-131-247-2
12	186	22.7	153	4	US-09-131-247-4
13	186	22.7	388	4	US-09-131-247-16
14	186	22.7	389	4	US-09-131-247-14
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16	183.5	22.4	178	4	US-08-862-730C-23
17	183.5	22.4	178	4	US-09-417-455-10
18	183.5	22.3	115	3	US-09-128-155-5
19	183.5	22.3	115	3	US-09-128-155-9
20	183.5	22.3	115	3	US-09-128-155-13
21	182.5	22.3	136	3	US-09-128-155-11
22	182.5	22.3	167	3	US-09-128-155-7
23	182.5	22.3	178	3	US-09-128-155-2
24	182	22.2	156	1	US-08-476-860-10
25	182	22.2	156	2	US-08-910-733-10
26	182	22.2	156	2	US-08-910-884-10
27	182	22.2	159	1	US-08-459-811-2

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29	182	22.2	159	2	US-08-092-092-2	Sequence 2, Appl1
30	182	22.2	159	2	US-08-459-814-2	Sequence 2, Appl1
31	182	22.2	159	2	US-08-425-232-2	Sequence 2, Appl1
32	182	22.2	159	2	US-08-471-227-3	Sequence 3, Appl1
33	182	22.2	159	2	US-08-479-140-2	Sequence 2, Appl1
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36	182	22.2	177	1	US-08-422-655-2	Sequence 2, Appl1
37	182	22.2	177	1	US-08-809-185-2	Sequence 2, Appl1
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ALIGNMENTS

RESULT 1
US-08-939-300-2
Sequence 2, Application US/08939300
Patent No. 5945310
GENERAL INFORMATION:
APPLICANT: Young, Peter R.
APPLICANT: James, Ian E.
TITLE OF INVENTION: Connor, Janice R.
TITLE OF INVENTION: A No. 5945310e1 Member of the IL-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939, 300
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046, 957
FILING DATE: May 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23, 031
REFERENCE/DOCKET NUMBER: GH-70018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-300-2
Query Match 55.3%; Score 452; DB 2; Length 164;
Best Local Similarity 94.6%; Pred. No. 1.6e-43;

Db 137 DMFIASSKRD-QPIILTSELGKSYNTAFELN 166

INVENTOR: Young, Robert M.
 APPLICANT: James, Ian E.
 APPLICANT: Connor, Janice R.
 TITLE OF INVENTION: A No. 5945310e1 Member of the IL-1

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1      RESULT      6
2      US-09-000-630C-21
3      ; Sequence 21, Application US/09000630C
4      ; Patent No. 6018029
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Fuller, Gerald M
7      ; APPLICANT: Fuentes, Nelson L.
8      ; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
9      ; TITLE OF INVENTION: Antagonist
10     ; NUMBER OF SEQUENCES: 27
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESS: Douglas C Murdock/ Bradley, Arant, Rose & White
13     ; STREET: 2001 Park Place, Suite 1400
14     ; CITY: Birmingham
15     ; STATE: Alabama
16     ; COUNTRY: USA
17     ; ZIP: 35203-2736
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Diskette, 3.50 Inch,
20     ; COMPUTER: IBM compatible
21     ; OPERATING SYSTEM: Microsoft Windows
22     ; SOFTWARE: Wordperfect 6.0
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/09/000.630C
25     ; FILING DATE:
26     ; PRIOR APPLICATION DATA:
27     ; APPLICATION NUMBER: 08/862,730
28     ; FILING DATE:
29     ; INFORMATION FOR SEQ ID NO: 21:
30     ; SEQUENCE CHARACTERISTICS:
31     ; LENGTH: 178 amino acids
32     ; TYPE: amino acid
33     ; STRANDEDNESS: single
34     ; TOPOLOGY: linear
35     ; MOLECULE TYPE: mouse IL-1ra sequence
36     ; US-09-000-630C-21

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Query Match      23.9%; Score 195.5; DB 3; Length 178;
Best Local Similarity 33.6%; Pred. No. 1.7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

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QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
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RESULT 7
US-08-862-730C-21
; Sequence 21, Application US/08862730C
; Patent No. 6063600
; GENERAL INFORMATION:
; APPLICANT: Puller, Gerald M.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Douglas C. Murdoch/ Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400
; CITY: Birmingham
; STATE: Alabama
; COUNTRY: USA
; ZIP: 35203-2736
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; OPERATING SYSTEM: Microsoft Windows
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,730C
; FILING DATE: 5/23/97
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mouse IL-1ra sequence
; US-08-862-730C-21

Query Match      23.9%; Score 195.5; DB 3; Length 178;
Best Local Similarity 33.6%; Pred. No. 1.7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAPKSAIRDSRQMWVWVLSGNSLIAPL-SRSIK-----PYTLHLIACRDTFRS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 KRCKMQAFRIWDTNOKTFYLRNNQLIAGYLGQPNIKLECKIDWVPIDLH----- 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 DKEGNMNYLIGIKGKDLCPAEIQGKPTLQLEKNIMDIYVEKKAOKPFLFFHNKESG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 -----SVFLGIGHGKLCCLCAKSGDDIKQLQLEEVNITDLSKNKEEDKRFTFIRSEK 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 TSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 8
US-09-417-455-9
; Sequence 9, Application US/09417455

```

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; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-417-455-9

Query Match      23.9%; Score 195.5; DB 4; Length 178;
Best Local Similarity 33.6%; Pred. No. 1.7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAPKSAIRDSRQMWVWVLSGNSLIAPL-SRSIK-----PYTLHLIACRDTFRS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 KRCKMQAFRIWDTNOKTFYLRNNQLIAGYLGQPNIKLECKIDWVPIDLH----- 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 DKEGNMNYLIGIKGKDLCPAEIQGKPTLQLEKNIMDIYVEKKAOKPFLFFHNKESG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 -----SVFLGIGHGKLCCLCAKSGDDIKQLQLEEVNITDLSKNKEEDKRFTFIRSEK 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 TSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 9
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 185

```

MOLECULE TYPE: protein

APPLICANT: Collins, David S.

